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Q7FNE2_ORYSA PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                               Name=msrmk2;
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avena sativ
triticum ae
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                                                                                              December 27, 2005, 20:29:56 ; Search time 230 Seconds (without alignments) 1128.845 Million cell updates/sec
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1 MDGAPVAEFRPTMTHGGRYL......DQMKQLIFNEAIEMNPNIRY 368
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                            Compugen Ltd.
             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compug
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                                                                                                                                                                                                                                                          2166443 seqs, 705528306 residues
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09F033_ORYSA

09FSE6_ORYSA

09FSE6_ORYSA

04QWQ7_SACOF

043079_AVESA

081599_WHEAT

09ZWJ6_MAIZE

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Q5PZV2 9BRAS
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Q4JKA8 9CARY
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Q8LT18_SOLTU
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MPK6_ARATH
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ARATH
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
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    protein search,

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08H0B1-09YSA
09XGY8 IPOBA
09XGY8 IPOBA
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084XZ PETCR
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ALIGNMENTS

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GO; GO:0004707; P:MAP kinase activity; IEA.

GO; GO:0004707; P:MAP kinase activity; IEA.

GO; GO:0004707; P:MAP kinase activity; IEA.

GO; GO:0004713; P:protein-tyrosine kinase activity; IEA.

InterPro; IPR00351; JNK MAPK.

InterPro; IPR00351; MAP kin.

InterPro; IPR00351; MAP kin.

InterPro; IPR00311; Ser Lhr Jkinase.

InterPro; IPR001245; Tyr Jkinase.

INTERPRO; PR001245; Tyr Jkinase.

R FRINTS; PR01772; JNKMAPKINASE.

R PRODO; PD000001; Prot kinase; 2.

R MART; SM00219; TyrKc; 1.

R SMART; SM00219; TyrKc; 1.

R PROSTIE; PS00117; PROTEIN KINASE ATP; 1.

R PROSTIE; PS00107; PROTEIN KINASE DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa (japonica cultivar-group).
Bukaryota, Vitidiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzaes, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
99.5%; Score 1942.5; DB 2; Length 369;
Best Local Similarity 99.7%; Pred. No. 2.9e-113;
Matches 368; Conservative 0; Mismatches 0; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              369 AA; 42995 MW; 417D81732635F2D3 CRC64;
                                                                                                                                                                                                            Last sequence update)
Last annotation update)
369 AA
                                                                                                                                               Created
                                                                                                                                05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
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9

1 MDGAPVAEFRPTWTHGGRYLLYDIFGNKFEVTNKYQPPIMPIGRGAYGIVCSVMNFETRE

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181 FGLARPSSESDWATEYVVTRWYRAPELLLNSTDYSAAIDVWSVGCIFMELINRQPLFPGR 240
                                                                                                                                                                                                                                                                                                                                                                                                                              MVAIKKIANAFUNDMDAKRTLREIKLLRHLDHENIIGIRDVIPPPIPQAFUDVYIATELM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 MVAIKKIANAFNNDMDAKRTLREIKLLRHLDHENIIGIRDVIPPPIPQAFNDVYIATELM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIDLAHIIRSNQELSEEHCQYFLYQILRGLKYIHSANVIHRDLKPSNLLLANANCDLKICD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 DIDLHHIIRSNQELSEEHCQYFLYQILRGLKYIHSANVIHRDLKPSNLLLNANCDLKICD 180
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                                                                                                                                                                                                                                                                                                                                1 MDGAPVAEFRPTWTHGGRYLLYDIFGNKFEVTNKYQPPIMPIGRGAYGIVCSVMNFETRE
                                                                                                                                                                                                                                                                                                                                                          1 MDGADVAEFRPTWITHGGRYLLYDIFGNKFEVINKYQPPIMPIGRGAYGIVCSVMNFETRE
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                                                                                                                                                                                                                                                                                  Gaps
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (1) — WUCLEOUIDE SEQUENCE. Song F., Goodman R.M.; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases. Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases. EMBL; ARX01710.1; -; mRNA. HSSP; Q16539; IXVI. Gramene; Q3AS; IXVI. Gramene; Q3AS; F:ATP binding; IEA. GO; GO:000524; F:ATP binding; IEA. GO; GO:0004707; F:MAP kinase activity; IEA. GO; GO:0004677; F:DCCtein serine/threonine kinase activity; IEA. GO; GO:0006468; P:proctein amino acid phosphorylation; IEA.
                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                              DB 2; Length 369;
                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                               42995 MW; 417D81732635F2D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                         99.5%; Score 1942.5; DB 2
99.7%; Pred. No. 2.9e-113;
iive 0; Mismatches 0;
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  ProDom; PD000001; Prot_Kinase; 2.
SMART; SM00220; S TKC; 1.
PROSITE; PS01351; MAPK; 1.
PROSITE; PS500107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
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InterPro; IRR008352; MAP_kin.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR008271; Ser_thr_pkin_AS.
InterPro; IPR002290; Ser_thr_pkinase.
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PRINTS; PR01772; JNKMAPKINASE.
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Q9AXF2;
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Matches 368; Conservative
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361 IEMNPNIRY 369
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                            MDGAPVAEFRPTWTHGGRYLLYDIFGNKFEVTNKYOPPIMPIGRGAYGIVCSVMNFETRE
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Oryza sativa (Rice).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gramene; OSFCM3; -.. Gramene; OSFCM3; -.. Gramene; OSFCM3; -.. GO: GO:0004707; F:ATP binding; IEA.
GO; GO:0004707; F:MAP kinase activity; IEA.
GO; GO:000468; P:protein serine/threonine kinase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR008351; JNK MAPK.
InterPro; IPR003227; MAP kin.
InterPro; IPR000719; Prof. kinase.
InterPro; IPR008271; Ser_thr pkin AS.
InterPro; IPR002290; Ser_thr pkin AS.
InterPro; IPR002290; Ser_thr pkin AS.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-FBB-2005 (TrEMBLrel. 29, Last annotation update)
MAP kinase 1 (MAP kinase MAPK5a).
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EMBL, AP216315; AAG40579.1; -; mRNA.
EMBL, AF479883; AAL87689.1; -; mRNA.
HSSP; Q16539; 1KV1.
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HSSP; Q16539; LKVI.
G2; G0:000524; FATP binding; IEA.
G9; G0:0004707; F:MAP kinase activity; IEA.
G9; G0:0004664; F:protein serine/threonine kinase activity; IEA.
G9; G0:0006468; P:protein amino acid phosphorylation; IEA.
G0; G0:0006488; P:protein amino acid phosphorylation; IEA.
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Trach
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
                                                                                                                                                                                                                                                                              Indels
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Wing R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Cur
Collura K.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AC134232; AAO16999.1; -; Genomic_DNA.
                            Prodom; PD000001; Prot_Kinase; 2.
SMART; SM00220; S TKC; 1.
PROSTIE; PS001035; MAPK; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE TY; 1.
SEQUENCE 369 AA; 42957 MW; 1E7BF2603BA2FD6B CRC64;
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Last annotation update)
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99.2%; Pred. No. 2.5e-112;
ive 0; Mismatches 2;
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GO; GO:0004707; F:MAP kinase activity;
GO; GO:0004674; F:protein serine/threon.
GO; GO:0006468; P:protein amino acid ph.
InterPro; IPR003551; JNK MAPK.
InterPro; IPR003527; MAP kin.
InterPro; IPR003527; Ser_thr.pkin. AS.
InterPro; IPR002290; Ser_thr.pkin. AS.
InterPro; IPR002290; Ser_thr.pkin.as.
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          PR01772; JNKMAPKINASE.
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                                                                                                                                                                                                                        Query Match 98.7%;
Best Local Similarity 99.2%;
Matches 366; Conservative
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Q8GZZ3;
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                                                                                                                                                                                                                                                                                   Gape
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Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ250311; CAC13967.1; -; mRNA.

RHSSP; Q16539; IKVI.

R Gramene; Q3FSE6; -.

GO; GO:0004707; F:ATP binding; IEA.

GO; GO:0004707; F:MAP kinase activity; IEA.

GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

GO; GO:0004674; F:protein amino acid phosphorylation; IEA.

R GO; GO:0004679; F:MAP kinase activity; IEA.

InterPro; IPR008351; JMR_MAPK.

InterPro; IPR008351; JMR_MAP.

InterPro; IPR00019; Prot kinase.

InterPro; IPR002290; Ser_thr_pkinase.

R InterPro; IPR002290; Ser_thr_pkinase.

R Pfam; PF00069; Pkinase; I.
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                99.3%; Score 1938.5; DB 2; Length
                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                               369 AA; 43029 MW; 417D88E32635F2D3 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                    Pred. No. 5.1e-113;
0; Mismatches 1;
ProDom; PD000001; Prot kinase; 2.
SMART; SM0220; S TKC; 1.
PROSITE; PS01351; MAPK; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00108; PROTEIN KINASE DOM; 1.
RAINASE SECULI, PROTEIN KINASE ST; 1.
Kinase.
SEQUENCE 369 AA; 43029 MW; 417D88832635
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Best Local Similarity 99.5%;
Matches 367; Conservative
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2004 (TrEMBLrel. 26,
MAPKZ protein.
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NUCLEOTIDE SEQUENCE.
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Q43379;
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Best Local Similarity
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01-OCT-2003 (
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                                                                                                                                                                                                                              NDMDAKRTLREIKLLRHLDHENIIGIRDVIPPPIPQAFNDVYIATELMDTDLHHIIRSNQ 132
                                                                                                                                                                                                                                                                            ELSEEHCQYFLYQILRGLKYIHSANVIHRDLKPSNLLLNANCDLKICDFGLARPSSESDM 192
                                                                                                                                                                                                                                                                                                                           MTEYVVTRWYRAPELLLNSTDYSAA-DVWSVGCIFMELINRQPLFPGRDHMHQMRLITEV 251
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Micogen-activated protein kinase.
Saccharum officinarum (Sugarcane).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Saccharum officinarum complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nogueira F.T.S., Schlogl P.S., Camargo S.R., Fernandez J.H., De Rosa V.E. Jr., Pompermayer P., Arruda P.; "SBNAC23, a member of the NAC domain protein family, is associated with cold herbivory and water stress in sugarcane."; Plant Sci. 169:93-106(2005).

EMBL, AY738652, AAW65993.1; -; mRNA.
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                                                                                                                                 2; Length 357;
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                                                                                                          357 AA; 41723 MW; EF6C054A76B3D8FE CRC64;
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                                                                                                                               Query Match 96.2%; Score 1878.5; DB 3
Best Local Similarity 99.7%; Pred. No. 2.7e-109
Matches 356; Conservative 0; Mismatches 0
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94.1%; Score 1837; Di
Best Local Similarity 94.1%; Pred. No. 1.1e
Matches 348; Conservative 11; Mismatches
Pfam; PP00069; Pkinase; 1.
PRINTS; PR01772; JNKMAPKINASE.
ProDom; P0000001; Prot. kinase; 2.
SWART; SM00220; S TKC; 1.
PROSITE; PS01351; MAPK; 1.
PROSITE; PS0107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE_DOM; 1.
KINASE.
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Q4QWQ7;
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RY TISSUE-Aleurone;
RA MEDLINE-95284341; PubMed=7766874;
RA MEDLINE-95284341; PubMed=7766874;
RA MEDLINE-95284341; PubMed=7766874;
RA WEDLINE-95284341; PubMed=7766874;
RA WILLY A.K., Philips A.L.;
RI "gibberellin regulated expression in oat aleurone cells of two kinases of that have homology to nap kinase and a ribosomal protein kinase.";
RI Plant MO1. Biol. 27:1043-1052(1995).
REMEL: X79993; CAA56314.1; -; mRNA.
REMEL: X56638; S56638
REMEL: X56638; S6638
REMEL: X6004707; F:MAP kinase activity; IEA.
RO; GO:0006468; P:protein amino acid phosphorylation; IEA.
RO; GO:0006468; P:protein amino acid phosphorylation; IEA.
RO; GO:0006468; P:protein amino acid phosphorylation; IEA.
RICEPRO: IPRO0327; MAP kin.
RICEPRO: IPRO0327; MAP kin.
RICEPRO: IPRO0327; MAP kin.
RICEPRO: IPRO0329; Ser_thr_pkinase.
REMEN: SMO0220; STRC; I.
REMER: SMO0220; STRC; I.
REMOSITE; PSCO117; PROTEIN KINASE ATP; I.
REMOSITE; PSCO117; PROTEIN KINASE ATP; I.
REMOSITE; PSCO101; PROTEIN KINASE DOM; I.
REMOSITE; PSCO101; PROTEIN KINASE ST; I.
REMENTED STATE PSCO101; PROTEIN KINASE ST; I.
REMENTED STATE PSCO101; PSCO
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae,
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Pred. No. 1.3e-105;
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RMLTENPLØRITVBEALDHPYLERLHDIADBPICLEPPSFDPEQKALNEDQMKQLIFNEA 359
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Gramens; Q9ZWJG; -...
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004707; F:MAP kinase activity; IEA.
GO; GO:0004707; F:MAP kinase activity; IEA.
GO; GO:0004707; F:MAP kinase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0016740; F:protein amino acid phosphorylation; IEA.
InterPro; IPR008351; JWR MAPR.
InterPro; IPR008351; JWR MAPR.
InterPro; IPR00871; Ser_thr_pkin_AS.
InterPro; IPR008271; Ser_thr_pkinase.
Pfam; PF0065; Pkinase; I.
PR01772; JWRWAPKINASE.
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                                          Length 369;
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MBDLINE=20055759; PubMed=10589<u>9</u>42; DOI=10.1007/8004380051115;
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Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Trach
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
PACCAD clade, Panicoideae, Andropogoneae, Zea.
                                          ; Score 1812.5; DB 2; Length; Pred. No. 3.7e-105; 20; Mismatches 12; Indels
42803 MW; D8DD351176978434 CRC64;
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91.1%;
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Q9ZWJ6;
                                        Query Match
Best Local Similarity 91.11
Matches 336; Conservative
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                                                                     1 MDGAPVAEFRPTWTHGGRPLLYNIFGNQPEITSKYQPPIMPIGRGAYGIVCSVMNFETRE
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                                             1 MDGAPVAEFRPTWTHGGRYLLYDIFGNKFEVTNKYOPPIMPIGRGAYGIVCSVMNFETRE
    Gaps
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;
Triticeae; Triticum.
NCBI_TaxID=4565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Blicitor - and A23187-induced expression of WCK-1, a gene encoding mitogen-activated protein kinase in wheat."; Mitogen-activated protein kinase in wheat."; Plant Mol. Biol. 40:921-933 (1999).

EMBL; AF079318; AAC28850.1; -; mRNA.
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004574; F:ATP binding; IEA.
GO; GO:0004674; F:Protein serine/threonine kinase activity; IEA.
GO; GO:000468; P:protein serine/threonine kinase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR008351; JMK MAPK.
InterPro; IPR008351; MAP_kin.
InterPro; IPR008271; Ser_thr_pkin_AS.
InterPro; IPR002290; Ser_thr_pkin_as.
InterPro; IPR002290; Ser_thr_pkinase.
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MEDLINE=99454541; PubMed=10527417; DOI=10.1023/A:1006263607135;
Takezawa D.;
    ä
    11; Indels
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Last annotation update)
    20; Mismatches
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ProDom; PD00001; Prot_Kinase; 2.
SMART; SM00220; S TKc; 1.
PROSITE; PS01351; WAPK; 1.
PROSITE; PS0011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
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081599;
01-NOV-1998 (TERMBLE) 08,
01-NOV-1998 (TERMBLE) 08,
01-OCT-2003 (TERMBLE) 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Triticum aestivum (Wheat).
    Conservative
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LELNPNFRY 369
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GO; GO:0005524; F:
GO; GO:0004707; F:
GO; GO:0004674; F:
GO; GO:0006468; P:
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KIANAFNNDMDAKRTLREIKLLRHLDHENIIGIRDVIPPPIPQAFNDVYIATELMDTDLH 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pisum sătivum (Garden pea).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Rabales; Fabaceae; Papillonoideae; Vicieae; Pisum.
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GO; GO:0004707; F:MAP kinase activity; IEA.
GO; GO:0004678; F:MAP kinase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
GO; GO:0006689; P:protein amino acid phosphorylation; IEA.
InterPro; IPR008351; JMK MAPK.
InterPro; IPR0003527; MAP kin.
InterPro; IPR000719; Prof_kinase.
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MEDLINE=21003323; PubMed=11117261; DOI=10.1023/A:1006434330381;
MATCOLO M.J., Carbonell J.;
MATCOLO M.J., Carbonell J.;
acid and expression of a pea MAP kinase gene induced by gibbe:
acid and 6-benzyladenine in unpollinated pea ovaries.";
Plant Mol. Biol. 44:177-186(2000).
EMBL; AFL53061; AAF73236.1; -; mRNA.
HSSP; Q16539; IKVI.
                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                          77.8%; Score 1519.5; DB 2; Length 371; 76.1%; Pred. No. 6.8e-87; cive 53; Mismatches 32; Indels 1;
                                                                                                                                                                                          SEQUENCE 371 AA; 42649 MW; 5A63E7F73A1F3F2C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
              Pfam; PF00069; PKinase; I.
PRINTS; PR01772; JNKMARKINASE.
ProDom; PD000001; Prot_Kinase; 2.
SMART; SM00219; TVK; 1.
SMART; SM00219; TVK; 1.
PROSITE; PS00131; MAPK; 1.
PROSITE; PS00101; PROTEIN KINASE ATP; 1.
PROSITE; PS00108; PROTEIN KINASE DOM; 1.
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 InterPro; IPR001245; Tyr_pkinase.
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                                                                                                                                                                                                                                                              Matches 274; Conservative
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Q9M6S1 PEA PRELIMINARY;
Q9M6S1;
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                                                                                                                                                                                                                                            Similarity
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Q9M6S1_F
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                                                                                                                                                                                           Gaps
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosida; eurosida I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine. NCBI_TaxID=3847;
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Tallcitor-activated mitogen-activated protein kinase(s) (MAPK) from
soybean (Glycine max L.).";

Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.

E Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.

R GO; GO: 000524; F-ATP binding; IEA.

R GO; GO: 00004707; F:MAP kinase activity; IEA.

R GO; GO: 00004707; F:MAP kinase activity; IEA.

R GO; GO: 00004708; F:protein serine/threonine kinase activity; IEA.

R GO; GO: 00004689; F:protein amino acid phosphorylation; IEA.

InterPro; IPR003527; MAP kin.

R InterPro; IPR003290; Ser_thr Janse.

R InterPro; IPR002290; Ser_thr Janse.

R InterPro; IPR008271; Ser_thr Jainase.

R InterPro; IPR008271; Ser_thr Jakinase.
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                                                                                                                                                    Query Match
90.8%; Score 1774; DB 2; Length 406;
Best Local Similarity 84.2%; Pred. No. 1e-102;
Matches 337; Conservative 18; Mismatches 13; Indels 3
                                                                                                                       CRC64;
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Mitogen-activated protein kinase 1.
              SMART; SM00220; S_TKC; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00109; PROTEIN KINASE DOM; 1.

PROSITE; PS00108; PROTEIN KINASE ST; UNKNOWN 1.

ATP-binding; Kinase; Nuclectide-binding;
Serims/threonine-protein kinase; Transferase.

SEQUENCE 406 AA; 46683 MW; E63A60A5C102A3F1
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PD000001; Prot_kinase; 2.
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QSK6Q4;
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NUCLEOTIDE SEQUENCE.
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371 AA;
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MUCLEOTIDE SEQUENCE.

MEDLINE=97008170; PubMed=8855346; DOI=10.1073/pnas.93.20.11274;

MEDLINE=97008170; PubMed=8855346; DOI=10.1073/pnas.93.20.11274;

MEDLINE=97008170; Hitth...

"signaling in plants: a mitogen-activated protein kinase pathway is activated by cold and drought.";

Proc. Natl. Acad. Sci. U.S.A. 93.11274-11279(1996).

PIR; T09622; T09622.
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Medicago.
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GO; GO:0004707; F:MAP kinase activity; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR00351; JNK MAPK.
InterPro; IPR003527; MAP_kin.
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                                                                                                                                                    DB 2; Length
                                                                                                                                                  Query Match 77.1%; Score 1505.5; DB 2; Length Best Local Similarity 74.7%; Pred. No. 5e-86; Matches 269; Conservative 55; Mismatches 35; Indels
                                                                                                                             SEQUENCE 371 AA; 42919 MW; A6F422D295CF488C CRC64;
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Last annotation update)
InterPro; IPR008271; Ser_thr_pkin_AS.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00069; Pkinase; I.
PRINTS; PR01772; JNKWAPKINASE.
ProDom; PD000001; Prot_kinase; 2.
SWART; SW00220; S TKC; 1.
PROSITE; PS01351; MAPK; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
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024077;
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69 KIANAFDNHAMDAKKTILREIKULRHIDHENVIGLRDVIPPPLRREFNDVYITTELMDTDLH 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MRLITEVIGTPTDDELGFIRNEDARKYMRHLPQYPRRTFASMFPRVQPAALDLIERMLTF 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NPLORITVEEALDHPYLERLHDIADEPICLEPFSFDFEQKALNEDOMKOLIFNEAIEMNP 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 VAEFPAVQTHGGQFVQYNVFGNLFEVTAKYRPPIMPIGRGAYGIVCSLLNTETNELVAVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 KIANAFUNDMDAKRTLREIKLLRHLDHENIIGIRDVIPPPIPQAFNDVYIATELMDTDLH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 VARFRPTWTHGGRYLLYDIFGNKFEVTNKYQPPIMPIGRGAYGIVCSVMNFETREMVAIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nicotiana tabacum (Common tobacco).

Eukaryoty, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamlids; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sano H., Yap Y.K.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
--- CATALTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
---- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; AB052964; BAB79636.1; ----; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; Q16539; IKVI.

GO; GO: 0005524; F:ATP binding; IRA.

GO; GO: 0004707; P:MAP kinase activity; IEA.

GO; GO: 0004707; P:Protein serine/threonine kinase activity; IEA.

GO; GO: 0006468; P:protein amino acid phosphorylation; IEA.

InterPro; IPR003527; MAP kin.

InterPro; IPR00719; Prof_kinase.

InterPro; IPR00719; Prof_kinase.

InterPro; IPR008711; Ser_thr_pkin_AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                       42963 MW; 8CCC390454E4350E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ol-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Wound induced protein kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35;
                                                                                                                                                                                                                                                                                                                                                                                                                77.0%; Score 1504.5; DB 74.4%; Pred. No. 5.8e-86;
InterPro; IPR000719; Prot_kinase.
InterPro; IPR00271; Ser_thr_pkin_AS.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PP00069; PKinase; I.
PRINTS; PR01772; JNKMAPKINASE.
SMORT; PD000001; Prot_kinase; 2.
SMART; SM00220; S TKC; I.
PROSITE; PS0135; MAPK; I.
PROSITE; PS01151; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         74.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 268; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8W406 TOBAC PRELIMINARY;
Q8W406;
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AIKKIANAFNNDMDAKRTLREIKLLRHLDHENIIGIRDVIPPPIPQAFNDVYIATELMDT 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LTFNPLQRITVERALDHPYLERLHDIADEPICLEPFSFDFEQKALNEDQMKQLIFNEAIE 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22795301; PubMed=12913131; DOI=10.1104/pp.103.024414; Holley S.R., Yalamanchili R.D., Moura D.S., Ryan C.A., Stratmann J.W.; "Convergence of signaling pathways induced by systemin, oligosaccharide elicitors, and ultraviolet-B radiation at the level of mitogen-activated protein kinases in Lycopersicon peruvianum suspension-cultured cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LARPSSESDMMTEYVVTRWYRAPELLLINSTDYSAA-DVWSVGCIFMELINRQPLFPGRDH
                                                                                                                                                                                                                                                                                                                                                                                       3 GAPVAEFRPTWTHGGRYLLYDIFGNKFEVTNKYOPPIMPIGRGAYGIVCSVMNFETREMV
                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                    DB 2; Length 370;
                                                                                                                                                                                                                                                                                                                                    40; Indels
                                                                                                                                                                                                                                                                     370 AA; 42594 MW; 84C29502FCB167B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-MDR-2004 (TrEMBLrel. 26, Last annotation update) Mitogen-activated protein kinase 3.
                                                                                                                                                                                                                                                                                                    75.8%; Score 1480.5; DB 73.8%; Pred. No. 1.8e-84; ive 54; Mismatches 40
InterPro; IPR003527; MAP kin.
InterPro; IPR003719; Prot kinase.
InterPro; IPR003290; Ser thr pkinase.
InterPro; IPR001245; Tyr pkinase.
Pfam; PR001245; Tyr pkinase.
PRINTS; PR0171; ERKSERK4MAPK.
PRINTS; PR01771; BRKSERK4MAPK.
PRINTS; PR01772; JNKMAPKINASE.
PRODOM; PR000001; Prot kinase; 1.
SWART; SM00220; S TKC; 1.
PR051TE; PS01151; MAPK; 1.
PR051TE; PS01151; MAPK; 1.
PR051TE; PS01151; MAPK; 1.
PR051TE; PS010109; PR0TEIN KINASE DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
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                                                                                                                                                                                                                                                                                                                                    Matches 268; Conservative
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Q84MI4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4081;
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                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yu. S., Zhang L., Zuo K., Tang D., Tang K.;
"Isolation and characterization of an oilseed rape MAP kinase BnMPK3 involved in diverse environmental stresses.";
Plant Sci. 169:413-421 (2005).
EMBL, AX642433, AAV34677.1; -; mRNA.
GO; GO:0005524; F:ARTP binding; IEA.
GO; GO:0004707; F:MAP kinase activity; IEA.
GO; GO:0004713; F:protein serine/threonine kinase activity; IEA.
GO; GO:0004713; F:protein serine/threonine kinase activity; IEA.
GO; GO:0004713; F:protein serine/threonine kinase activity; IEA.
InterPro; IPR008350; BrA 3 4 MAPK.
InterPro; IPR008350; BrA 3 4 MAPK.
                                                                                                                                                                                                                                                      Gaps
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Brasrycia, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosida; eurosida II; Brassicales; Brassicaceae; Brassica.
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                                                                                                                                                                                                                     2; Length 375;
                                                                                                                                                                                                                                                  42; Indels
                                 PRINTS; PRO1773; P38MAPKINASE.
Probom; PD000001; Prot_Kinase; 2.
SMART; SM00200; S_TKc; 1.
PROSITE; PS01351; MAPK; UNKNOWN 1.
PROSITE; PS01101; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN KINASE ST; 1.
ATP-binding; Kinase; Wucleotide-binding; Kinase; Serine/threonine-procein kinase; Transferase.
SEGUENCE 375 AA; 42898 MW; 9BA49C8C39EIC88F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Mitogen-activated protein kinase 3.
                                                                                                                                                                                                                    Query Match 75.9%; Score 1481.5; DB 3 Best Local Similarity 73.0%; Pred. No. 1.6e-84; Matches 265; Conservative 55; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 370
      InterPro; IPR002290; Ser thr pkinase.
Pfam; PF00069; Pkinase; 1.
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6 MGAAQFPDFPKIVTHAGQYVQYDIFGNLFEITNKYQPPIMPIGRGAYGIVCSVFNAELNE 65...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 DTDLHQIIRSNQGLSEDHCQYFWYQLLRGLKYIHSAHVIHRDLKPSNLLLNANCDLKICD 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186 FGLARPNVENENMTEYVVTRMYRAPELLINSSDYTAAIDVWSVGCIFMELMNRKPLFAGK 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIDLAHIIRSNQELSEEHCQYFLYQILRGLKYIHSANVIHRDLKPSNLLLNANCDLKICD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 FGLARPSSESDMMTEYVVTRWYRAPELLINSTDYSAA-DVWSVGCIFMELINRQPLFPGR 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 DHMHQMRLITEVIGTPTDDELGFIRNEDARKYMRHLPQYPRRTFASMFPRVQPAALDLIE 299
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11. Plant Physiol. 132:1728-1738(2003).

2. -- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

3. C. -- SMILARITY: Belongs to the Ser/Thr protein kinase family.

3. RMEL; AYZel114; AAPZ0421.1; -; mRNA.

3. RMEL; AYZel114; AAPZ0421.1; -; mRNA.

3. RO; GO:0004707; F:MAP kinase activity; IEA.

4. GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

5. GO:0004674; F:protein serine/threonine kinase activity; IEA.

5. GO:0004674; F:protein serine/threonine kinase activity; IEA.

5. GO:0004674; F:protein serine/threonine kinase activity; IEA.

6. GO:0004674; F:protein serine/threonine kinase activity; IEA.

7. GO:0004674; F:protein serine/threonine kinase activity; IEA.

8. GO:0004674; F:protein serine/threonine kinase activity; IEA.

8. RO; GO:0004674; F:protein serine/threonine-trotein kinase; IEA.

8. RO; GO:0004674; F:protein kinase; IEA.

8. RRSITE; PSO0101; PROTEIN KINASE DOM; I.

8. RROSITE; PSO0104; PROTEIN KINASE DOM; I.

8. RROSITE; PSO0104; KINASE; NUCLEOLIGE-binding; KINASE; TARABELERE TRANSEE TEARSEUCCESAT CRC64; SEQUENCE 373 AA; 42797 MW; 80625A5CROCCE547 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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LALNP 370
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Search completed: December 27, 2005, 20:40:24 Job time : 233 8ecs

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                  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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	Description	CL961355 OBIFCC006	CB675228 OSJNEelON	CB675229 OSJNEe10N	CK163044 FGAS01565	BE412950 MCG016.H0	BM817317 HC108A05	DR792177 ZM BFb001	CN130436 RHOH1 41	CA213307 SCQGSB114	CK077805 81986rsic	C99344 C99344 Rice	CF243446 3530 1 21	AL504341 AL504341	BI805515 S040D07 S	CF985761 23806rsic	CO527096 3530 1 17		CA272118 SCVPLB208	CA150824 SCBFRZ204	BB412824 MCG008.C0	AL503490 AL503490	CN143831 WOUND1_18
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CK207629 FGAS01927 CA485025 WRB4313_E DR811341_ZM BFb003 CA159385 SCJFRZ3CO DR781175 ZM BFb000 CN110591 RH0H1 42 CO731261 JBW019E02 CR22274 CR292374 CR292374 CR292374 CV071886 EST4047 ZCK199849 FGAS00835 CA494243 WHB4304_A DR972294 ZM BFb000 CR199845 RFGM0052 CA160578 SCJTR3307 CK201815 FGAS01033 BF622856 HYSME3000 AY108471 Zea may8 BQ839433 WHE4166_A AU091538 AU091538 BJ281984 BJZ81984	ALIGNMENTS CL961355 1074 bp DNA linear GSS 21-SEP-2004 OBIFCCO06068 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence. CL961355.1 GI:52377449 GSS. Oryza sativa (indica cultivar-group) Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poaceae;	X., Su,N., Li,L., Wang,X., Cao,M., o,J., Sun,D., Zhao,H., Yuan,L., ng,J. I regulation of the rice genome and Beijing 101300, China	iva (indica cultivar-group)" NA" 6" tima Express Library" exon trapped genomic sequences "	76.8%; Score 1072.4; DB 10; Length 1074; ; Conservative 0; Mismatches 1; Indels 0; Gaps 0; ATGACGCACGGCCGGTACCTGCTTCGGCAACAACTTCGAGAGGTCGAGGGGGGGG
CK207629 CA485025 DR811341 CA153385 DR713591 CO731261 DR813762 CV071886 CK292974 CK2029485 CK20113 CK09485 CK201815 CK201815 CK201815 AM1084781	ALIGNMENTS 1074 bp sativa Express comic, genomic s 7449 a cultivar-grou antae; Streptop coliophyta; Lili	.C., Liu y.C., Liu y.X., Ba y.X., Ba riptiona bidopsis bidopsis canatic Genomics iences,	ers sat c D 3994	Score 1072.4; Pred. No. 4.9 0; Mismatches PACCTGCTCTACGAC
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44444WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW	CL961355 OSIFCC006068 Oryza 6 Cultivar-group) genc CL961355.1 GI:52377 GSS. GSS. Oryza sativa (indic Oryza sativa (indic Bukaryota; Viridiple Spermatophyra; Magna	1 (bases 1 to 1044) Ma,L., Wangc,J., Chen Jiao,Y., Sun,N., Zhan Wong,G.K.S., Deng,X.W. An analysis of transc: its comparison to Aral Unpublished (2004) Contact: Chen Chen Department of Bioinfo Beijing Institute of Chinese Academy of Fax: 86-10-80481559 Fax: 86-10-80481559 Fax: 86-10-80481559 Fax: 10-604888676	Class: exc	Similarity 3; Conser ATGACGCAC
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Oryga sativa (japonica cultivar-group)

Oryga sativa (japonica cultivar-group)

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;

Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;

Ehrhartoideae; Oryzeae, Oryzeae.

I (bases 1 to 755)

S Jantasuriyarat.C., Gowda, M., Haller.K., Hatfield, J., Lu, G.,

Stahlberg, E., Zhou, B., Li, H., Kim, H., Yu, Y., Dean, R.A., Wing, R.A.,

Soderlund, C. and Wang, G.L.

Large-scale identification of expressed sequence tags involved in

rice and rice blast fungus interaction

ID 15888683
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/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; 24 hrs after innoculation with Rice Blast (70-15)"
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OSJNEe10N07.f OSJNEe Oryza sativa (japonica cultivar-group) cDNA clone OSJNEe10N07 5', mRNA sequence.
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/organism="Oryza sativa (japonica cultivar-group)"
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/olitivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNRE10N07"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH109"
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                                                                                                                                                                                                                                                                                 Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Bo
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
                                                                                                                                                                                                                                                                                                                                                                                                                             FORWARD: gra aaa cga cgg cca gtg
BACKWARD: gga aac agc tat gac cat g
Plate: 10 row: N column: 07
Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                   Email: rwing@genome.arizona.edu
PCR PRimers
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Library 4 Gate 8 Triticum
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                                                                                                                           ö
/lab_host="DH10B"
/clone_lb="OSJNRe"
/note="Vector: pBluescript II KS +; Site_1: EcoR1; Site_2:
Xho1; 24 hrs after innoculation with Rice Blast (70-15)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               392 GATGCTCACCTTCAACCCGCTGCAGAGAATCACAGTTGAGGAGGGGGGCGCTCGATCATCCTTA 333
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                                                                                                                           Gaps
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                                                                                          Length 752;
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                                                                                          53.6%; Score 748.8; DB 6; 99.7%; Pred. No. 2.7e-164; ive 0; Mismatches 2;
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Triticum aestivum
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Matches 750; Conserv
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Oryza sativa (japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Enhartoideae; Oryzeae; Oryza.

Stantautiyarat, C., Gowda, M., Haller, K., Hatfield, J., Lu, G.,

Stantautiyarat, C., Gowda, M., Kim, H., Yu, Y., Dean, R.A., Wing, R.A.,

Soderlund, C. and Wang, G.L.

Large-scale identification of expressed sequence tags involved in rice and rice blast fungus interaction

L. Plant Physiol. 138 (1), 105-115 (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OSJNEELONO7.r OSJNEE Oryza sativa (japonica cultivar-group) cDNA clone OSJNEELONO7 3', mRNA sequence.
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                                       GTCAGAAGAGCACTGCCAGTATTTCCTGTACCAGATCCTGCGGGGGCTCAAGTACATCCA
                                                                                            CTCGGCGAACGTGATCCACCGCGACCTGAAGCCGAGCAACTGCTGCTGAACGCCAACTG
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Corganism="Oryza sativa (japonica cultivar-group)"

/mol type="mcNa"

/mol type="mcNa"

/cultivar="Nipponbare"

/db xref="taxon.39947"

/clone="OSJNBelloN07"

/tissue_type="Leaf"

/dev_stage="3 week"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson,
85721-0088, USA
Tel: 520 628 3967
Pax: 520 621 9288
                                                                                                                                                                                                                                                                                                                                                                                                       GACGCCGACGGACGACGAGCTGGGGTTCATACGGA 873
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: rwing@genome.arizona.edu
PCR PRimers
FORWARD: gta aaa cga cgg cca gtg
BACKWARD: gga aac agc tat gac cat g
Plate: 10 row: N column: 07
Seg primer: gga aac agc tat gac cat g.
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Hordeum vulgare

Hordeum vulgare

Hordeum vulgare

Hordeum vulgare

Hordeum vulgare

Hordeum vulgare

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Pooideae; Triticeae; Hordeum.

B. (bases 1 to 863)

S. Anderson, O.A., Appels.R., Balley,P., Blake,T., Close,T.,
Cloutier,S., Dubcoveky,J., Feuillet,C., Gale,M., Graner,A.,
Gustafson,P., Herrmann,R.G., Holton,T., Jacquemin,J.N., Jia,J.,
Joudrier,P., Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P.,
Ogilhara,Y., Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G.,
Shariflou,M., Sorrells,M., Warburton,M. and Wenzel,G.
International Triticeae EST Cooperative (ITEC): Production of
Expressed Sequence Tags for Species of the Triticeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BE412950 863 bp mRNA linear EST 24-JUL-2000 MCG016.H09R990625 ITEC MCG Barley Leaf/Culm Library Hordeum vulgare CDNA clone MCG016.H09, mRNA sequence.
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                                                    CGTCTACATCGCCACCGAGCTCATGGACACGACCTCCACCACCATCATCGCTCCAACCA
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International Triticeae EST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Graner A
Institute for Plant Genetics & Crop Plant F
Corrensetr. 3, D-06466 Gatersleben GERMANY
Tel: 49 39482 5521
Fax: 49 39482 5137
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                                                                                                                                                                                                                                                                University of Saskatchewan, Department of Computer Science
1C101 Engineering Building, 57 Campus Drive, Saskatoon,
Saskatchewan, S7N 5A9, Canada
1C101 Engineering Building, 57 Campus Drive, Saskatoon,
Tel: 306 966 1769
Fax: 306 966 2033
Email: fgas ests@cs.usask.ca
This sequence is the direct result of the Base calling software
This sequence is the direct result of the Base calling software
This sequence is the direct result of the Base calling software
This sequence is the direct result of the Base calls. To aid in the identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified the region [40, 815].
Plate: L4B066 row: O column: 18.
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Spoideae; Triticum.

1 (Dases; Triticae; Triticum.
1 (Dases; Lot 1031)
Allard, F., Crosby, W.L., Danyluk, J., Budes, F., Frick, M., Gaudet, D., Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Larochie, A., Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilson, D., Penniket, C., Roach, J.L. and Sanhan, P. Unpublished (2003)
Contact: Wm L Crosby
Bioinformatics
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51.9%; Score 725; DB 7; Length 1031;
Best Local Similarity 88.0%; Pred. No. 1e-158;
Matches 821; Conservative 0; Mismatches 109; Indels
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/dew_stage="etiolated"
/clone_lib="ITEC MCG Barley Leaf/Culm Library"
                                                                                                               47.9%; Score 668.2; DB 2; Length 863;
llarity 89.6%; Pred. No. 2e-145;
Conservative 0; Mismatches 83; Indels 0
Location/Qualifiers
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Hordeum vulgare subsp. vulgare

Hordeum vulgare subsp. vulgare

Hordeum vulgare subsp. vulgare

Hordeum vulgare subsp. vulgare

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Pooideae; Triticeae; Hordeum.

E 1 (bases 1 to 916)

S Ozturk, N.Z., Michalowski, C.B., Brazille, S., Borchert, C.,

Palacio, C., Normand, C., Murphy, C., Kelley, R., Sant, S.A.,

McLaughlin, H., Fredricksen, M.A. and Bohnert, H.J.

Monitoring large-scale changes in transcript abundance in droughtand salt-stressed barley

Contact: Mark A. Fredricksen BM817317 BOT THE BOT BOT BOT THE BOT OS-MAR-2002 HC108A05 SK.abl HC Hordeum vulgare subsp. vulgare cDNA clone HC108A05_SK.abl similar to Methylumbelliferyl-acetate deacetylase, Thymidylate kinase, Polynucleotide adenylyltransferase, BM817317 4 189 309 369 429 /organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/mol_type="mRNA"
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/sub_species="vulgare"
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Query Match
Best Local Similarity
Matches 708; Conserv
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/organism="Zea mays"
/organism="Zea mays"
/organism="Zea mays"
/orltivar="B73"
/db_xref="taxon:4577"
/tissue type="mixed (silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo)"
/dev stage="varies by tissue"
/lab_host="DH10B T1 phage resistant"
/clone_lib="ZBA BFb"
/note="Vector: pCWV-SPORT 6.1; Site_1: ECORV; Site_2:
Note; Maize Full length cDNA library
/created by Invitrogen from multiple tissues; Organ: silks,
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1 (Dases 1 to 921)

Kim, H., Collura, K., Wissotski, M., Smart, D., Kudrna, D., Muller, C., Masok, K., Haller, K., Wing, R., Soderlund, C., Walbot, V. and Yu, Y.
Unpublished (2005)
               ACTGCCAGTACTTCCTGTACCAGCTGCTGCGGGTCTCAAGTACATCCACTCGGCGAACG
                                                                                                                                                                                                                                                                                                                                                                 768 CCCGGGGAAGGACCCCATGCACCAAGATGCGCTCATCACGGGAGTGATCGGGACCCCCAC
                                                                                                                                                                                                                                                                                                                                                                                                848 GGACGACGAGCTGGGGTTCA-TACGGAACGAGAACGCGAGGAAGTACATGA-GGCACCTG
ACTGCCAGTATTTCCTGTACCAGATCCTGCGGGGGCTCAAGTACATCCACTCGGCGAACG
                                                                                TCTGCGACTTCGGGCTGGCGCGCCGTCGTCGGAGAGCGACATGATGACGGAGTACGTGG
                                                                                                                                                                                               TCACGCGGTGGTACCGGGCCCCCGGAGCTGCTCTAACTCCACCGACTACTCCGCCGCC
                                                                                                                                                                                                                                                                                 TCTGCGACTTCGGCCTGGCGCGCGCGTCGGAGAGCGACATGATGACGGAGTACGTGG
                                                                                                                                                                                                                                                                                                                                CCCCGGCAGGGACCACATGCACCAGATGCGCCTCATCACCGAGGTGATCGGGACGCCGAC
                                                                 TGATCCACCGCGACCTGAAGCCGAGCAACCTGCTGCTGAACGCCAACTGCGACCTCAAGA
                                                                                                                                                                                                                                                                ATCGACGTCTGGTCCGTCGGCTGCATCTTCATGGAGCTCATCAACCGC-CAGCCGCTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2M BFb0011021.r ZM_BFb Zea maye cDNA 5', mRNA sequence. DR792177 GI:71311501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Yeisoo Yu
Arizona Genomics Institute
The University Of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 520 626 9585
Fax: 520 621 1259
Email: yeisooogenome.arizona.edu
Plate: 0011 row: O column: 21.
Location/Qualifiers
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diversity of the seed so that set is using recombination rather than restriction enzymes. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of CDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurons; 4. inmature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the seedlings; 10. 10 dap whole seed; Arizona clones, high density filters and amplified library can be ordered from the University of Arizona the University of Arizona the University of Arizona (http://www.genome.arizona.edu/orders/)."

GCGGCGAGAGAAGAGGAGGATTAGGGATGGACGGGCGCCCGGTGGCGGAGTTCAGG Gaps ; 0 Length 921; IndelB 8, 89; Score 654.6; DB 8; Pred. No. 3.1e-142; 0; Mismatches 89; 46.9%; 708; Conservative

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167 124 GCCCCGAGGAAGAAGATGAGCGGAGGAGGCGTGGACGGAGCTCCGGTCGCCGAGTTCCGG 183 243 CCGACGATGACGCACGCCGGCCGGTACCTGCTCTACGACATCTTCGGGAACAAGTTCGAG CAGACGGTGACGCCACGGCCGGTTCCTGCAGTACAACATCTTCGGCAACCTGTTCGAG

TGCTCGGTGATGAACTCCGAGACGAGAGAGATGGTGGCCATCAAGAAGATGGCCAACGCC 363 347 TICGACAACCACATGGGCCCAAGGGCACGCTCCGGGAGATCAAGCTGCTGAGGCACCTC 423 TTCAACAACGACATGGACGCCAAGCGCACGCTCCGGGAGATCAAGCTCCTCAGGCACCTC

407 483 GACCACGAGAACATCATCGGCATCAGGGACGTGATCCCGCCGCCCCGTCCCGCAGGCGTTC GACCACGAGAACATCATAGGCATCAGGGATGTGATCCCGCCGCCGCGGATCCCTCAGGCGTTC

AACGACGTGTACATCGGGACGGAGCTGATGGACACGGACCTGCACCACCACATCATCCGGTCC AACGACGTCTACATCGCCACGGAGCTCATGGACACCGACCTCCATCACATCATCGCCTCC

467 543 527 603 587 663 647

AACCAGGAGCTCTCGGAGGAGCACTCCCAGTACTTCATGTACCAGATCCTCGGGGGCTC AACCAAGAACTGTCAGAAGAGCACTGCCAGTATTTCCTGTACCAGATCCTGCGGGGGCTC

604 AAGTACATCCACTCCGCCAACGTGATCCACCGCGACCTCAAGCCCAGCAACCTGCTG **AACGCCAACTGCGACCTCAAGATCTGCGACTTCGGGCTGGCGCGCCGTCGTCGGAGAGC** AAGTACATCCACTCGGCGAACGTGATCCACCGCGACCTGAAGCCGAGCAACCTGCTGCTG

GACATGATGACGGAGTACGTGGTCACCCGGTGGTACCGCGCCGGAGCTGCTGCTCAAC 707

GACATGATGACGGGTACGTGGTCACGCGCTGGTACCGCGCGCCCCGAGCTGCTGCTCAAC 783

us-10-768-886-1.rst

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2000 tax 10 mod 2000; 1
gl_A002 Acid- and alkaline-treated roots Sorghum clone RHOH1_41_B01_A002 5', mRNA sequence.
Eukāryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
<pre>clade; Panicoideae; Andropogoneae; Sorghum. 1 (bases 1 to 859) Cordonnier-Pratt,MM., Suzuki,Y., Sugano,S., Klein,R.R., Liang,C.,</pre>
<pre>cman,A. and Fract, L.H. id- and alkaline-treated roots</pre>
Laboratory for Genomics and Bioinformatics The University of Georgia, Department of Plant Biology
2, Athens, GA 30602-7271, USA
Email: mmpratt@uga.edu Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
repared at Texas A & Milversity; for Genomics and Bloinformatics,
vector and regions below bired quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to
NOTAGE (CTTCTGCTCTAAAAGCTGCG). hr: Sugs (CTTCTGCTCTAAAAGCTGCG). Location/Qualifiers
Or"
mol_type="mtN4" foulfivar="BTx623" foulfivar="BTx628"
2" e-resistant E. coli"
<pre>lkaline-treated roots" tor: pWE185-FL3; Site 1: XhoI;</pre>
ry was prepared from polyA+ MNA rvested from BTx623 sorghum
oponic culture. HCl was added to a ings, KOH to a pH of 9.0 for
others. Koots were harvested 3, 12 and 2/ hr arter addition and pooled for RNA preparation. Double-stranded CDNA was cloned undirectionally into different Draili sites of the pMR185-FL3 vector (5-prime Draili site is
II site is CACCATGTG). XhoI excises
Score 623.2; DB 7; Length 859; Pred. No. 6.8e-135; O. Mismarrhes 73: Indels 105: Gans 1:

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ITCAACCCGCTGCAGAATCACAGTTGAGGAGGCGCT 1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                718 bp mRNA linear EST 25-SEP-2003
harum officinarum cDNA clone SCQGSB1140A09
                                                                                                                        SOCCCTACGGGATCGTCTGCTCCGTGATGAACTTTGA 247
                                                                                                                                                                                                                                                                                                                  CCGATCCCTCAGGCGTTCAACGACGTCTACATCGCCAC 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCGAGCAACCTGCTGCAACGCCAACTGCGACCTCAA 607
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                                                            TCGGGAACAGTTCGAGGTGACGAACAAGTACCAGCC 187
                                                                                                                                                                                    AGAAGATCGCCAACGCGTTCAACAACGACATGGACGC 307
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 127
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GCATCTTCATGGAGCTCATCAACCGCCAGCCGCTCTT
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CK077805 612 bp mRNA linear BST 05-FEB-2005 81986rsicen 10007.yl Oryza sativa cv. LYP9 booting whole plant cDNA library Oryza sativa (indica cultivar-group) cDNA 5', mRNA
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Yu,J., Wang,J., Lin,W., Li,S., Li,H., Zhou,J., Ni,P., Dong,W.,
Hu,S., Zeng,C., Zhang,J., Zhang,Y., Li,R., Xu,Z., Li,S., Li,X.,
Zheng,H., Cong,L., Lin,L., Yin,J., Geng,J., Li,G., Shi,J., Liu,J.,
Li,J., Wang,J., Deng,Y., Ran,L., Shi,X., Wang,X., Wu,Q.,
Li,C., Ren,X., Wang,J., Wang,X., Li,D., Liu,D., Zhang,X., Ji,Z.,
Zhao,W., Sun,Y., Zhang,Z., Bao,J., Han,Y., Dong,L., Ji,J., Chen,P.,
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Oryza sativa (indica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        767 CATCAACCGCCAGCCGC-TCTTCCCCGGCAGGGACCACATGCCACCAGATGCGCCTCAT 823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  661 CATCNAACCGCAGCCGCTTCTTTCCCGGACGCGACCATGCACCAGATGCGCCTCAT 718
                                                                                                                                                                                                                                                 GAACGCCAACTGCGACCTCAAGATCTGCGACTTCGGGCTGGCGCGCCGTCGTCGAGAG
                                                                                                                                                                                                                                                                                                                                  481 GAACGCCAACTGCGACCTCAAGATCTGCGACTTCGGGCTGGCGCGCCCCCTCCTNCGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCCACCGACTACTCCGCCGCCATCGACGTCTGGTCCGTCGGCTGCATCTTCATGGAGCT
                                                                                                                                                        421 CAAGTACATCCACTCCGCCAACGTGATCCACCGCGACCTCAAGCCCAGCAACCTGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                          CGACATGATGACGGAGTACGTGGTCACCCGGTGGTACCGCGCCGGAGCTGCTGCTCCAA
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    .632
/organism="Oryza sativa (indica cultivar-group)"

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The Genomes of Oryza sativa: A History of Duplications
PLOS Biol. 3 (2), e38 (2005)
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Hangzhou Genomics Institute
No.51 Zhijisng Road, Hangzhou 310008, China
Tel: 86-571-56805886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43.6%; Score 608; DB 7; L 99.5%; Pred. No. 2.4e-131; iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:39946"
/tissue_type="whole plant"
/dev_stage="booting"
/clone_lib="Oryza sativa cv
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Seq primer: M13 Forward
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/cultivar="LYP9"
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The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Genet. Arruda P
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estedual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Gollection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 140 row: A column: 09
Seq primer: T7 Promoter Primer.
                                 Saccharum officinarum
Saccharum officinarum
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, Lillopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Saccharum, Saccharum officinarum
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/mol_type="mRNA"
/mol_type="mRNA"
/clone="SCCGSB1140A09"
/lab_host="DH10B"
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CFZ43446 819 bp mRNA linear BST 06-AUG-2003 3530 1 21 1 COL.y 1 3530 - Full length cDNA library created by Invitrogen from multiple tissues Zea mays cDNA, mRNA sequence. CF243446
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
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        /organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
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/cultivar="Nipponbare"
/db xref="taxon:39947"
/clone="E10732_8Z"
/dev stage="ripening stage"
/clone=lib="Rice panicle at ripening stage"
/note="Organ: panicle; Rice cDNA from panicle at ristage"
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Best Local Similarity 99.8%;
Matches 607; Conservative
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Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Vandiophyta; Liliopsida; Poales; Poaceae;
Ehrhatcoldeae; Oryzeae; Oryza.
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Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasaxi@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
PROJECT = 'RGP'
POLYA-No.
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                                                                               264 TGCTCGGTGATGAACTCCGAGAGGAAGATGGTGGTGGCCCATCAAGAAGAAGAACCCC
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/db_xref="taxon:112509"
/clone="HW04P17V"
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/cultivar="Barke"
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//dev_stage="waries by tissue"
/lab host="bullob"
/lab host="bullob"
/lab host="bullob"
/lone lib="3530 - Full length cDNA library created by
/notce="Organ: ailks, husks, ears, pollen, shoot tips,
leaf, root tips, whole seed, embryo; Vector: pGWV-SPORT
6.1; Site_1: EcoRV; Site_2: Not!; Maize Gene Discovery
Project contracted with Invitrogen to produce a
normalized, full length library in a pSport vector. This
is a Gateway compatible vector, permitting clone movement
to new vector backbones for expression in diverse host
cells using recombination rather than restriction enzymes.
Details of the vector and sequencing primers are available
at ZmDB in the EST library description tables. poly(A)+
mRNA was prepared by Invitrogen, and equimolar amounts of
RNA from each of the 12 tissue samples were mixed together
for selection of mRNA with a 5' cap. After synthesis of
cDNA, a normalization step was conducted against the
mixture of RNA sources. This step effected a 20x reduction in common transcript types. Tissues prepared: 1
just emerging silks; 2. inner husks from ears of sample
#1; 3. 20 dap aleurone; 4. immature tassels, stages from
1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm
vegetative shoot tips from 15 day old seedlings; 10. 10 dap whole seed; 11.
12 day endosperm and embryo; 12. 17 dap endosperm and
embryo. All of the sequenced clones in project 3530 will
be archived at the University of Arizona along with the
Unigene clones from the Agaened clones in project 3530 will
sequencing project Clones can be ordered through the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCGCCGAGAGAAGAGGAGGGAATTAGGGATGGACGGGGCGCCCGGTGCCGGAGTTCAGG 107
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ZmDB web site or directly from the University of Arizona
(http://www.genome.arizona.edu/orders/). High density
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                                                                                            University
Unpublished (1999)
Contact: Walbot V
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
761: 650 723 227
Rax: 650 725 8221
Email: Walbot@stanford.edu
Plate: 3530 1 21 row: C column: 01.
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Best Local Similarity 88.7%; Pred. No. 2.4e-130; Matches 653; Conservative 0; Mismatches 83;
Panicoldeae; Andropogoneae; Zea
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                                                                                                                                                                                                                                                                                                                                                                                              /organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
                         (bases 1 to 819)
                                           Walbot, V
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Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.

E losses 1 to 700)
Michalek, W., Weschke, W., Ploissner, K.-P. and Graner, A.

EST sequencing and analysis in barley
L Unpublished (2000)
Contact: Michalek W
Institute for Plant Genetics and Crop Plant Research
Cortenset: 3, D-06466 Gateraleben, Germany
Email: michale@ibk-gatersleben.ge, http://pgrc.ipk-gatersleben.de
Seq primer: T3 primer for 5'end.
AL504341 Hordeum vulgare Barke roots Hordeum vulgare subsp. vulgare cDNA clone HW04P17V 5', mRNA sequence.
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ORGANISM
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/tissue_type="roots"

/lab host="xtofk"

/lab host="xtofk"

/clok"

/cloke="letc-ribasmid pBK-CMV; Site_1: EcoRI; Site_2:

/note="Vector: plasmid pBK-CMV; Site_1: EcoRI; Site_2:

/note="Wearter than the content of a paring barley variety

/barke', a high quality malting variety. Roots were grown

for two days on filter paper at room temperature cloning

sites: EcoRI (5'-end of cDNA) and XhoI (3'-end of cDNA).

NOTE: Due to a cloning artefact caused by the kit, in most

cases the EcoRI site is NOT present, as well as the EcoRI

adapter. Average insert size is 1 kb Sequence trimming:

Vector sequences and sequence ends were trimmed from the

5'-and 3'-end until a 50 bp window contains less than two

ambiguities. The maximum length was set to 700 bp"
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BI805515 667 bp mRNA linear BST 02-OCT-2001 S040D07 Stem library from Oryza sativa (3-5 leaf stage) Oryza

RESULT 14 BI805515 LOCUS DEFINITION

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                                                                                             Oryza sativa
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Bhrhartoideae; Oryzaea; Oryza,
1 (bases 1 to 667)
Dong, H.T., Li, D.B., Zhuang, X.F., Dai, C.G., Sun, L.X., Pei, Y.X., Wu, H.F., Jiang, Y.X., Yu, F.C., Gao, Q.K. and Lou, Y.C.
A Gene Expression Screen in Oryza sativa
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/dev stage="3-5 leaf stage"
/clone_lib="Stem library from Oryza sativa (3-5 leaf
stage)"
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                                                                                                                                                                                                                                                                          Contact: Haitao Dong, Debao Li
Bioinfomatics and Gene Network Research Group
Zhejiang University
Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China
Tel: 0086-571-86892051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 594.2; DB 3;
Pred. No. 4.1e-128;
0; Mismatches 8;
sativa cDNA clone S040D07, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Oryza sativa"
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                                                                                                                                                                                                                                                                                                                                                                              Fax: 0086-571-86961525
Email: webmasterGestarray.org, U
Seq primer: M13 forward primer.
Location/Qualifiers
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/clone="S040D07"
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BI805515.1 GI:15852719
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Search completed: December 29, 2005, 07:45:40 Job time : 4047 secs
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Oryza sativa (indica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bhrhartoideae; Oryzae; Oryza
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| Organism="Oryza sativa (indica cultivar-group)" |
| mol Lype="mRNA" |
| cultivar="Lype="mRNA" |
| db_xref="taxon:39946" |
| tissue Lype="whole plant" |
| dev_grage="tillering" |
| clone lib="Oryza sativa cv. LYP9 tillering whole plant |
| cDNA library" |
                                                                            538 -TIGCATITGTITGTITGTIGATGTITGGAAACCCACATITCTCTGCAAGITGTGGGCTGCTI
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                                               1268 ATTGCATTTGTTTGTTGATGTTCGAAACCCACATTCTCTGCAAGTTGTGGCTGCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Yan Zhou
Bioinformatics Department
Hangzhou Genomics Institute
No.51 Zhijisang Road, Hangzhou 310008, China
Tel: 86-571-56805886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: zhouyan@genomics.org.cn
Seq primer: M13 Forward
High quality sequence stop: 625
POLYA=No.
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AUTHORS
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ACGCCGCCCGCTACCTCCTACGACATCTTCGGGAACAAGTTCGAGGTGACGAACAAGT
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December 29, 2005, 02:45:39; Search time 617 Seconds (without alignments) 15079.272 Million cell updates/sec
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
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4	808.4	57.9	1084	13	ADT02331	Adt02331 Rice mito
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12	185.8	34.8	1520	13	ADX53699	Adx53699 Plant ful
13	184.2	34.7	1546	ო	AAC43674	Aac43674 Zea mays
14	484	34.7	1544	~	AAV27563	Aav27563 Salicylic
15	183.6	34.6	1119	4	AAC84253	Aac84253 Signal tr
16	183.2	34.6	1725	7	AAT60349	Aat60349 MAP kinas
17 4	167.8	33.5	1888	13	ADX11753	Adx11753 Plant ful
18	148.4	32.1	1786	~	AAT60350	Aat60350 MAP kinas
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                                            The invention relates to a rice mitogen-activated protein kinase 5 (MAPKS) polypeptides and the polymucleotides encoding them. The invention also relates to an antibody that specifically binds to a peptide consisting of a C-terminal portion of a MAPKS polypeptide, a transgenic plant transformed by a polymucleotide encoding a MAPKS orthologue where ever expression of the MAPKS orthologue in the plant results in increased tolerance to abiotic stress comparated to a wild-type plant and a method for evaluating a plant for tolerance to abiotic stress comprising for evaluating a plant for tolerance to abiotic stress comprising in MAPKS activity in the plant where the increase in MAPKS activity in the plant where the increase in MAPKS activity in the plant where the increase in MAPKS activity in the plant to abiotic stress. The methods and compositions of the present invention are useful for increasing tolerance to abiotic and biotic stress in plants using MAPKS, where the abiotic tress is drought, temperature or salinity and the biotic stress is from pathogenic bacteria, viruses, nematodes and insects. This sequence represents cDNA encoding the rice MAPKSa polypeptide of the invention.
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ive 0; Mismatches 0;
                Claim 1; SEQ ID NO 1; 36pp; English.
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Best Local Similarity 100.
Matches 1396; Conservative
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RR 13-ULL-1999; 99US-0144624P.
RR 14-ULL-1999; 99US-0144062P.
RR 15-ULL-1999; 99US-0144062P.
RR 16-ULL-1999; 99US-0144062P.
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RR 21-ULL-19904.
PORCOLL 1999; 99US-0149904P.
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Best Local Similarity 87.8%; Pred. No. 1.8e-179;
Matches 1004; Conservative 0; Mismatches 140; Indels
9905-0157117P

9905-01573P

9905-0158029P

9905-0158232P

9905-0159294P

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                                                                                                               CCCGGACGCGACACACACACACAGATGCGCCTCATAACCGAGGTGATCGGGACGCCCACG
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                         487 GTGATCCACCGCGACCTCAAGCCCAGCAACCTGCTGGTGAACGCCAACTGCGACCTCAAG
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GTGATCCACCGCGACCTGAAGCCGAGCAACCTGCTGCTGAACGCCAACTGCGACCTCAAG
                                                                                          ATCTGCGACTTCGGGCTGGCGCGCCGTCGTCGGAGGCGACATGATGACGGAGTACGTG
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                                                                                                                                                                                                                          New signal transduction nucleic acids and encoded proteins useful for regulating phytohormone expression, including ethylene, auxins, cytokinins and gibberellin, to provide control of plant response to
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Pred. No. 1.3e-178;
0; Mismatches 127; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1125 BP; 241 A; 390 C; 317 G; 177 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 89-90; 126pp; English.
                                                                     (PION-) PIONEER HI-BRED INT INC
    99US-0134292P.
99US-0142996P.
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Best Local Similarity 88.7°
Matches 992; Conservative
                                                                                                                                                                                                                                                                                                stresses.
                                                                                                                                                           WPI; 2001-031929/04.
                                                                                                                                                                                P-PSDB; AAB48046.
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                         08-JUL-1999;
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GATTGAATCACCATGGAAATGAGATCCCGTCTATACCTGCTTTGTACATATGATCAAGAT 1246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates a recombinant DNA construct comprising a polymucleotide having any of 5544 nucleotide sequences (CDNAs SEQ ID NO: 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences (SEQ ID NO: 5545-11088). The CDNAs and proteins are from corn, soybean, Arabidopsis, wheat and rape but the specification does not indicate which sequences is derived from which organism. Also included is a method of producing a plant having an improved property, comprising transforming a plant havense to construct comprising a promoter region
                                                                                                                                                                                                                                                                                                                       CTCTGCAAGTIGIGGCTGCTTTGTATGATATGGTACTATGTTCGAATAAAAGGGTTTG 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New recombinant DNA constructs useful in the field of biochemistry and genetics, and in particular for producing transgenic plants with improved biological characteristics.
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drought tolerance; disease resistance; galactomannan production;
plant growth regulator; heat tolerance; herbicide tolerance;
lignin production; extreme osmotic condition tolerance;
pathogens resistance; pest resistance; yield improvement; seed oil yield;
                                                                     CCAAATGAAGCAGCTGATCTTCAACGAAGCGATCGAGATGAACCCAAACATCCGGTACTA
                                                                                                                                                                                                                                                                                     CTCTGCAAGTTGTGGCTGCTTTGTATGATATATGGTACTATGTTCGAATAAAAGGGTTTG
                                                                                         GATTGAATCACCATGGAAATGAGATCCCGTCTATAACCTGCTTTGTACATATGATCAAGAT
                                                                                                                                                                                                                                      reagcccarcrecregascccrrcrccrrcsacrrcsascassasscrrraaacsassas
                                                                                                                                                                                                                                                                                                                                                            GAACTITGGATTAAAAAAAAAAAAAAA 1396
                                                                                                                                                                                                                                                                                                                                                                                 GAACTITGGATTAAAAAAAAAAAAAAAAA 1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 5013; 14pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-APR-2003; 2003US-00424599.
28-APR-2003; 2003US-00425115.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plant cDNA, Seq ID 5013.
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1067
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ADT19687
ID ADT1
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                                                                                                                                                                                                                                                                                                  The invention relates to a rice mitogen-activated protein kinase 5 (MARKS) polypeptides and the polymucleotides encoding them. The invention also relates to an antibody that specifically binds to a peptide consisting of a C-terminal portion of a MARKS polypeptide, a transgenic plant transformed by a polymucleotide encoding a MARKS orthologue where over expression of the MARKS orthologue in the plant results in increased to clerance to ablotic stress comparated to a wild-type plant and a method for reating a plant for tolerance to ablotic stress comprising treating a plant with ablotic stress, isolating a MARKS portein from the plant, detecting MARKS activity and evaluating the increase or decrease in MARKS activity in the plant where the increase in MARKS activity confident to ablotic stress. The methods and compositions of the present invention are useful for increasing tolerance to ablotic and blotic stress in plants using MARKS, where the ablotic stress is allowed the biotic stress is from pathogenic bacteria, viruses, nematodes and insects. This sequence pathogenic bacteria, viruses, nematodes and insects. This sequence
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                                                                                                                                                                                             New isolated nucleic acid molecule encoding a mitogen-activated protein kinase-5 (MAPK5) polypeptide, useful for increasing tolerance to abiotic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 57.9%; Score 808.4; DB 13; Length 1084; Local Similarity 99.9%; Pred. No. 1.5e-156; es 809; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1084 BP; 262 A; 288 C; 316 G; 218 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                      Claim 11; SEQ ID NO 3; 36pp; English.
31-JAN-2003; 2003US-0444249P.
                                                                                                                                                                                                                                  and biotic stress in plants.
                                                                                                                         2004-747214/73.
                                                                                                                                                               GENBANK; AF479884.
                                                                                         Yang Y, Xiong L;
                                 (YANG/) YANG Y.
(XION/) XIONG L.
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c functional in a plant cell operably joined to a polynucleotide encoding a polypeptide associated with the property, and growing the transformed collypeptide associated with the property, and growing the transformed collypant coll tolerance. For manipulating growth rate in plant cells by modification of the cell cycle pathway, for improving plant drought tolerance, for providing increased complex tolerance to plant disease, for improving plant tolerance to hardicides, for increasing the rate of improving plant tolerance to extreme osmotic conditions, for improving plant tolerance to extreme osmotic modification of carbohydrate, nitrogen or phosphorus use and/or uptake and for yield improvement by providing improved plant growth and development under at least one stress condition. The polynucleotide may also encode a plant transcription factor. The methods and compositions of the present invention are useful in the field of biochemistry and compositions are useful in the field of biochemistry and biological characteristics such as increased yield, improved nitrogen flow, increasing plant tolerance to cold or heat, improving plant colerance to extreme osmotic and drought conditions, and improving plant colerance to plant bereding markers, computer-based storage and carrays of molecules, plant breading markers, computer-based storage and carrays of molecules, plant breading markers, computer-based storage and carrays of molecules, plant begenes are some of the 5544 plant collarance to extreme osmotic and experses or pathogens.
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Sequence 1837 BP; 393 A; 594 C; 477 G; 373 T; 0 U; 0 Other;

112 432 672 172 232 292 612 352 412 732 CGTCTACATCGCCACCGAGCTCATGGACACGGACCTCCACCACAGCATCCGTTCCCGCAA 792 433 GATGACGCACCCGGCCGCTTCCTCTTACAACATATTCGGCAACCAGTTCGAGATCAC 492 552 CGTCTACATCGCCACGGAGCTCATGGACACCGACCTCCATCACATCATCCGCTCCAACCA 472 AGAACTGTCAGAAGAGCACTGCCAGTATTTCCTGTACCAGATCCTGCGGGGGCTCAAGTA 532 CATCTCCACGCCACTCGTGCGCCGCCACCGACGTCTGGTCCGCCAGCTGCATCTTCATGC 912 CAACAACATGGACGCCAAGCGCACGCTCCCGGGAGATCAAGCTCCTGAGGCCACCTCGACCA GAGAGAAGAGGAGGAGGATTAGGGATGGACGGGGCGCCGGTGGCGGAGTTCAGGCCGAC GAGAGTTTCGTGGCCGTGTTTGAGAATGGACGCGCTCGGGTGGCCGAGTTCCGGCCGAC GATGACGCACGCCGCCCGGTACCTGCTCTACGACATCTTCGGGAACAAGTTCGAGGTGAC GGCCAAGTACCAGCCGCCGATCATGCCCCATCGGCCGCGCGCCTACGGGATCGTCTGCTC CGTGATGAACTTTGAGACGAGGGAGATGGTGGCGATAAAGAAGATCGCCAACGCGTTCAA GGTGATGAACTTCGAGACGAGGAGATGGTGGCAATCAAGAAGATCGCAAACGCTTTCGA CAACGACATGGACGCCAAGCGCACGCTCCGGGAGATCAAGCTCCTCAGGCACCTCGACCA CGAGAACATCATAGGCATCAGGGATGTGATCCCGCCGCCGATCCCTCAGGCGTTCAACGA GAACAAGTACCAGCCGCCCATCATGCCCCATTGGCCGCGCGCCTACGGGATCGTCTGCTC Gaps Query Match
44.6%; Score 623.2; DB 13; Length 1837;
Best Local Similarity 70.9%; Pred. No. 2.1e-118;
Matches 892; Conservative 0; Mismatches 343; Indels 23; 373 493 473 793 533 23 113 173 233 553 293 613 353 673 413 733 853 ઠે 셤 ₹ 셤 ઠે 셤 ò 요 ò 셤 ઠ g ઠે 셤 ò 셤 ò

	GATGACGGAGTACGTGGTCACCCGGTGGTACCGCGCGCCGGAGCTGCTGC 702	GCACGGGGGTGATCTGCACCCCGCCGACGACGACCCCGATTCACCCGGACGAGGAC 1032	TCAACTCCACCGACTACTCCGCCATCGACGTCTGGTCGGTC	GCCAGGAGGTACATGAGGCACTGCCGCAGTTCCCTCGCGGTCCTTCCCAGGGCCAGTT 1092	AGTCATCAACCGCCAGCGCTCTTCCCGGCAGGGACCACATGCACCAGATGCGCCT 820	CCCCAAGGIGCAGCCCGCCGCGCTGGCACCTCATCGAGAGGATATTCACCTGATACGGCT 1152	CATCACCGAGGTGATCGGGACGCCGACGACGACGACTGGGGTTCATACGGAACGAGGA 880	TATCACGGATGTCATCGGCACCCCCACCGACGACTGGGTATAATCCGGAACGAGGA 1212	CGCGAGGAAGTACATGAGG-CACCTGCCGCAGTACCCGCGCCGGACGTTCGCGAGCATGT 939	GGCCAGGAGGTACATGAGGCCACCTGCCGCGGTTCCCTCGCCGGTCCTTCCCGGGACAGT 1272	TCCCGCGGGGTGCAGCCCGCCGCCTCGACCTCATCGAGATGCTCACCTTCAACCCGC 999	TCCCCAAGGTGCAGCCCGCCGCGCTGGACCTCCATCGAGGATGCTCACCTTCAACCCGC 1332	TGCAGAGAATCACAGTTGAGGAGGCGCTCGATCATCCTTACCTAGAGAGATTGCACGACA 1059	TGCAGAGGATCACAGTTGAAGAGGCGCTGGAGCACCCATACCTAGAGCGGCTTCACGACG 1392	TGGCGGATGAGCCCATCTGCCTGGAGCCCTTCCTCCTTCGACTTCGAGCAGAAGGCTCTAA 1119	TCGCCGACGACCCATCTGCACGGACCCCTTCTCCTTCGACTTCGAACAGCACCCACTGA 1452	ACGAGGACCAAATGAAGCAGCTGATCTTCAACGAAGCGATCGAGATGAACCCAAACATCC 1179	CGGAAGACCAGATGAAGCAGCTCATATTCAACGAAGCCCTGGAGTTGAACCCCAACTTCC 1512	GGTACTAGATIGAATCACCATGGAAATGAGATCCCGTCTATACCTGCTTT 1229	GATACTAGACGATTCATTCCTAGTTACCCCCAATAGTATGATTTCGATGTAACTGTTTG 1572	GTACATATGATTGAGATTGAGAGCGGGTAGACTGAACATTGCATTTGTTTTGTT 1287	TAAATAGGAGTAAGGTCAAAGAACATGGTAGATTGCGCACTGCATTTGTTTG	
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ADO84444 standard; cDNA; 873 (first entry) 21-APR-2005 ADO84444; RESULT 6 AD084444

BP.

Plant full length insert polynucleotide segid 3164.

plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotific condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield; protein content; gene; ss.

Unidentified

19-FEB-2004.

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1136
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                                                                                                                                                                                                                                                                        481 GAAGAGGCGCTGGAGCACCCGTACCTGGAACGGCTACACGACGTCGCCGACGACGACCATC
                                                                                                                                                                                                                                                                                                                                                                                        541 TGCACGGACCCGTTCTCGTTCGACTTCGAGCAGCTCTGACGGAAGACCAAATGAAG
GCCGCGCTCGACCTCATCGAGGATGCTCACCTTCAACCCGCTGCAGAGAATCACAGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
1. .197
/*tsg= a /product= "signal transduction protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal transduction protein encoding cDNA.
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P-PSDB; AAB48048.
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08-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention describes a recombinant DNA construct comprising a polymucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at available in electronic form from the US patent office at the legislation of the construct is useful for form from the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme common pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, combination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one strong sease condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens pests, for conferring increased resistance to plant disease, or for improving yield.
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Pred. No. 5.8e-102;
0; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                             Screen SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 3164; 15pp; English.
         28-APR-2003; 2003US-00425114.
                                                                                                                                                                                                                                                                                                                                                             Kovalic DK,
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89.3%;
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Matches 585; Conservative
                                                                                                                                                 LIU J.
ZHOU Y.
KOVALIC D K.
SCREEN S E.
TABASKA J E.
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further be used for recombinant expression of their encoded polypeptides, as immunogens in the preparation or screening of antibodies, and in sense or antisense suppression of genes in a host cell, tissue or plant. The proteins may be used in assays for enzyme agonists or antagonists, as immunogens or antigens to obtain antibodies specifically immunoreactive with the proteins. The present sequence represents a cDNA encoding a signal transduction protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGCCGAGCAACCTGCTGCTGAACGCCAACTGCGACCTCCAAGATCTGCGACTTCGGGCTG
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Pred. No. 9.2e-96;
0; Mismatches 355; Indels
                                                                                                                                                                 Seguence 1197 BP; 317 A; 306 C; 281 G; 293 T; 0 U; 0 Other;
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Matches 739;
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                                                            1000 ACTITIGAICCIAGACAGAGAATAACIGIIGAAGGCGCACTIGCACGICTITACIIGGCA 1059
                                                                                                                                                                        CAGAAGGCTCTAAACGAGGACCAAATGAAGCAGCTGATCTTCAACGAAGCGATCGAGATG
ACCTICAACCCGCTGCAGAGAATCACAGTTGAGGAGGCGCTCGATCATCCTTACCTAGAG
                                                                                                                                    AGATTGCACGACATCGCCGATGAGCCCCATCTGCCTGGAGCCCTTCTCCTTCGACTTCGAG
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auxin; cytokinin; gibberellin; immunogen; 88.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/product= "signal transduction protein"
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P-PSDB; AAB48047.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                            GCATCACTTCATGACATAAGTGATGAGCCAGCTGCTCAATGCCCTTCAGCTTTGACTTC
                                                                                                                                           GAGCAGAAGGCTCTAAACGAGGACCAAATGAAGCAGCTGATCTTCAACGAAGCGATCGAG
                                                              GAGAGATTGCACCACATCGCCCATCAGCCCCATCTGCCTGGAGCCCTTCTCCTTCGACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana DNA fragment SEQ ID NO: 38047.
                                                                                                                                                                                                                       1164 ATGAACCCAAACATCCGGTA 1183
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or antisense suppression of genes in a host cell, tissue or plant. The proteins may be used in assays for enzyme agonists or antagonists, as immunospens or antigens to obtain antibodies specifically immunoreactive with the proteins. The present sequence represents a cDNA encoding a signal transduction protein of the invention
                                                                                                                                                                                                                                                                   160 AACATCTTCGGCAACGTGTTCGAGGTCACCGCCAAGTACAAGCCCCCCGGTCCTCCCCATC
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36.6%; Score 511.2; DB 4; Length 1197;
Best Local Similarity 67.2%; Pred. No. 2.2e-95;
Matches 739; Conservative 0; Mismatches 358; Indels 3;
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The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid are representative of expressed polymucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polymucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants. Cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thalians stress regulated gene (ABZ12196-ABZ17574) used not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
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                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana; plant; gene; stress; transgenic;
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26-JAN-2001; 2001US-0264647P.
22-JUN-2001; 2001US-0300111P.
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    Length
                                              Indels
  Score 508.8; DB 3;
Pred. No. 6.7e-95;
0; Mismatches 357;
  Query Match
Best Local Similarity 67.2%;
Matches 736; Conservative
Query Match
Best Local Similarity
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Plant full length insert polynucleotide segid 22355.

21-APR-2005 (first entry)

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ADX47615 standard; cDNA; 1637 BP.

RESULT 11

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The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at try. seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, heaticides, extreme cancer conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, increased resistance to plant disease, for producing galactomannan, inginin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one treas condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert of the information in the recombinant DNA construct of the
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                                                                                                                         plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactoranana production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield; protein content; gene; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens pests, for conferring increased resistance to plant disease, or for
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05-NOV-2001; 2001US-00985678.
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KOVALIC D K.
SCREEN S E.
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The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at available in electronic form from the US patent office at the polynucleotide of the inspection are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme cosmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, ignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, introgen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one structure. This sequence represents a plant full length insert content. This sequence represents a plant full length insert of the plant can be used in the recombinant DNA construct of the
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                                                                                                                                       plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; heatied tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield; protein content; gene; ss.
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05-NOV-2001; 2001US-00985678.
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SCREEN S E.
TABASKA J E.
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Score 485.8; DB 13; Length 1520; Pred. No. 3.8e-90; 0; Mismatches 392; Indels 0;

14.8%; al Similarity 64.8%; 721; Conservative (

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05-MAR-1999;
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Hybridisation assay, genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic; pathway; promoter; termination sequence; corn; ss.
                                                                                              Zea mays DNA fragment SEQ ID NO: 40086.
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Location/Qualifiers

129. .1310 /*tag= a

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Salicylic acid induced protein; SIP; mitogen-activated protein; MAP; tobacco; disease resistance; microbial pathogen; MAP kinase; ds.
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                                            Salicylic acid induced MAP kinase encoding cDNA
22-SEP-1998 (first entry)
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(RUTF) UNIV RUTGERS STATE NEW JERSEY.

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96US-0029805P, 97US-00837593, 97WO-US019219

25-OCT-1996

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                                                This cDNA encodes a salicylic acid induced protein (SIP) kinase. This SIP kinase is an unique member of the mitogen-activated protein (MAP) kinase family. The salicylic acid induced MAP kinase of the invention comprises kinase subdomains I to XI of serine/Lhreonine kinases. The protein is activated by an agent that induces a disease defence response in plants by way of a signal transduction pathway that is at least partially dependent on salicylic acid. Host plant cells transformed with a vector containing a recombinant DNA molecule encoding the salicylic acid induced MAP kinase is used to produce the protein recombinantly. The products can he used to produce with increased disease resistance. The products may also be used as a research tool to identify other proteins involved in the hypersensitive response and systemic acquired response in plants
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Pred. No. 9e-90;
0; Mismatches 375; Indels
Claim 11; Page 21-22; 97pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 34.7%;
Best Local Similarity 65.6%;
Matches 722; Conservative
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AAV27563 standard; cDNA; 1544

RESULT 14

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The invention provides Zea mays signal transduction proteins and encoding nucleotide sequences. The nucleic acids are useful for regulating expression of phytohormones, including ethylene, auxins, cytokinins, and gibberellin, to effect developmental changes in plants and provide control of plant response to environmental stresses. They may also be used as probes or amplification primers in the detection, quantitation or isolation of gene transcripts, for detection mutations in the gene, for monitoring upregulation of expression or changes in enzyme activity in screening assays of compounds, for detection of any number of allelic variants, or for site-directed mutagenesis in eukaryotic cells. They may further be used for recombinant expression of their encoded polypeptides, as immunogens in the preparation or screening of antibodies, and in sense
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or antisense suppression of genes in a host cell, tissue or plant. The proteins may be used in assays for enzyme agonists or antagonists, as immunogens or antigens to obtain antibodies specifically immunoreactive with the proteins. The present sequence represents a cDNA encoding a signal transduction protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GITGCGAICAAGAAGGITGGCAATGCGITCCACAACCACATCGACGCCAAGCGGACGCTC
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                                                                                                                                                                                                                                                                                                                                                                                       New signal transduction nucleic acids and encoded proteins useful for regulating phytohormone expression, including ethylene, auxins, cytokinins and gibberellin, to provide control of plant response to
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mays; maize; signal transduction protein; phytohormone; ethylene;

auxin; cytokinin; gibberellin; immunogen; ss.

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/cgn2_6/ptodata/1/ina/PE_COMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-828-313-8
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US-08-176-620A-1
US-08-461-985-1
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ALIGNMENTS

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Sequence 1, Application US/09623034

Patent No. 6765128

GENERAL INFORMATION:

APPLICANT: Klessig, Daniel F.

APPLICANT: Klessig, Daniel F.

TITLE OF INVENTION: METHODS OF USING A PATHOGEN-ACTIVATABLE

TITLE OF INVENTION: MAP KINASE TO ENHANCE DISEASE RESISTANCE IN PLANTS

TITLE OF INVENTION: MAP KINASE TO ENHANCE DISEASE RESISTANCE IN PLANTS

FILE REPERRECE: RUT98-0073

CURRENT APPLICATION NUMBER: DCT/US99/03882

PRIOR FILING DATE: 1999-02-23

PRIOR PLING DATE: 1999-02-24

PRIOR FILING DATE: 1999-02-24

NUMBER OF SEQ ID NOS: 2

SOFTWARE: FREESE FOR Windows Version 3.0
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Best Local Similarity 65.6%;
Matches 722; Conservative
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  ; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-837-593-1
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GENERAL INFORMATION:
APPLICANT: COSTA & SILVA, OSWALDO DA
APPLICANT: COSTA & SILVA, OSWALDO DA
APPLICANT: THIELEN, NOCHA VAN
APPLICANT: CHEN, ROUYING
APPLICANT: CHEN, ROUYING
TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED PROTEINS AND METHODS OF
TITLE OF INVENTION: USE IN PLANTS
FILE REFERENCE: 16313-0032
CURRENT PILING DATE: 2001-04-06
FRIOR APPLICATION NUMBER: 60/196,001
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 128
COPTHANDS
CONTHANDS

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US-09-828-313-21
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SEQ ID NO 21
LENGTH: 1718
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Best Local Similarity 63.9
Matches 672; Conservative
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969 AGACTCCAAAAGCCCTTGACCTGGACCGGATGTTAACCTTTAACCCCAATAAACGGAT 1028
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                                                                                                                                                                                                                                                                                                                                               609 CCTTAAGATTTGTGATTTCGGCCTGGCCCGGATTGCCGATCCTGAGCATGACCACACCGG
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                                                                                  482 AGAAGAGCACTGCCAGTATTTCCTGTACCAGATCCTGCGGGGGCTCAAGTACATCCACTC
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| Patent No. 6271210
| GENERAL INFORMATION:
| APPLICANT: Sivaraman, Vimala S.
| APPLICANT: Wang, Haien-Yu
| APPLICANT: Wang, Haien-Yu
| APPLICANT: Walbon, Craig C.
| TILLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR MITC
| TILLE OF INVENTION: ANTISENSE AS THERAPY FOR CANN
| TILLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES
| TILLE REFERENCE: Seq. 1-4 (178-25 CIP II/CON)
| CURRENT APPLICATION NUMBER: US/09/412,289
| CURRENT PILLING DATE: 1999-08-12
| EARLIER FILING DATE: 1997-04-01
| EARLIER FILING DATE: 1997-04-01
| EARLIER FILING DATE: 1997-04-01
| EARLIER FILING DATE: 1997-03-28
| WUNBER OF SEQ ID NOS: 4
| NUMBER OF SEQ ID NOS: 4
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US-09-412-289-1
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                                                                                                                              APPLICANT: Vimala S. Sivaraman
APPLICANT: Helen-Yu Wang
APPLICANT: Craig C. Malbon
TITLE OF INVENTION: ANTISENSE OLIGONUCLECTIDES FOR MITOGEN-
TITLE OP INVENTION: ACTIVATED PROTEIN KINASES AS THERAPY FOR
TITLE OP INVENTION: BREAST CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1866
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Pred. No. 1.1e-64;
0; Mismatches 363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for windows
SOFTWARE: Mord Perfect 6.1 for windows
TLING DATE: August 12, 1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/909,742
FILING DATE: April 1, 1997
FILING DATE: April 1, 1997
FILING DATE: March 28, 1997
ATPOINTY/ACENT INFORMATION:
NAME: Adams, Lindsay S.
REGISTRATION NUMBER: 36,425
REFERENCE JOOKET NUMBER: 178-225 CIP II
TELEFONMUNICATION INFORMATION:
TELEFAK: (516) 822-3550
TELEFAK: (516) 822-3550
INFORMATION POR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann & Baron, LLP
STREET: 350 Jericho Turnpike
                                           Sequence 1, Application US/08909742
Patent No. 6007991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 24.2%;
Best Local Similarity 61.3%;
Matches 603; Conservative
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STRANDEDNESS: double
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                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              New York
                                                                                                                                                                                                                                                                                                                                                                                                CITY: Jericho
STATE: New YOU
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                              US-08-909-742-1
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Sequence 38, Application US/09417197

Patent No. 6518021

GENERAL INFORMATION:

APPLICANT: Old THASTRUP, et al.

TITLE OF INVENTION: On A Cellular Response

FILE REFERENCE: 3759-0110P

CURRENT APPLICATION UNDER: US/09/417,197

CURRENT FILING DATE: 1999-10-07

NUMBER OF SEQ ID NOS: 143

SOSTWARE: PATENT OF VERSION 3.0
996 cracreccaececacecrecesasariceaearecrececerrececerreaearer 1055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.2%; Score 337.2; DB 3; Length 1896; 61.3%; Pred. No. 1.1e-64; cive 0; Mismatches 363; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: EGFP-Erkl fusion construct
                                                                      1130 AATGAAGCAGCTGATCTTCAACGA 1153
                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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US-09-417-197-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1896
                                                                                                                                                                                       RESULT 6
US-09-417-197-38
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Matches 603;
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; OTHER INFORMATION: Description of Artificial Sequence:blank
US-09-412-289-1
                                                                                                                                                                                                                                                                                   CCAGCCGCCCATCATGCCCATTGGCCGCGCGCCCTACGGGATCGTCTG(
                                                                                                                                                                                    Score 337.2; DB 3;
Pred. No. 1.1e-64;
0; Mismatches 363;
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Best Local Similarity 61.3%;
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LENGTH: 1866
TYPE: DNA
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Parent No. 686731

GENERAL INFORMATION:
APPLICANT: COSTA e SILVA, OSWALDO DA
APPLICANT: COSTA e SILVA, OSWALDO DA
APPLICANT: THIELEN, NOCHA VAN
APPLICANT: CHEN, ROUYING
TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED PROTEINS AND METHODS OF
TITLE OF INVENTION: USE IN PLANTS
FILE REPERENCE: 16313-0032
CURRENT APPLICATION NUMBER: 05/196,001
FRIOR PPLICATION NUMBER: 60/196,001
PRIOR PPLICATION NUMBER: 60/196,001
                                                                                                 363 IGTTCAGGACCTCATGGAGACAGACCT---GTACAAGCTGCTTAAAAGCCAGCAGCTGAG 419
                                                                                                                                                                                          420 CAATGACCACATCTGCTACTTCCTACCAGATCCTCCGGGGCCTCAAGTATATACACTC 479
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Patent No. 6518021
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
On A Cellular Response
FILE REFERENCE: 3759-0110P
CURRENT APPLICATION NUMBER: US/09/417,197

CURRENT FILING DATE: 1999-10-07

NUMBER OF SEQ ID NOS: 143

SOFTWARE: Patentin version 3.0
1712
                                                                                                                                                                                                      CATCCTGGGCTCCCCATCCCAGGAGCCTGAATTGTATCATCAACATGAAGGCCCGAAA 1592
                                                                                                                                                                                                                                                                                                                                                   GCAGCCCGCCGCGCTCGACCTCATCGAGAATGCTCACCTTCAACCCGCTGCAGAGAAT 1009
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                                                                     CAACCGCCAGCCGCTCTTCCCCCGGCAGGACCACATGCACCAGATGCGCCTCATCACCGA
                                                                                                                  crcraaccedecentricecrededadeacraecredareacereaceacarrenge
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Pred. No. 5.7e-64;
0; Mismatches 365; Indels 18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: MERK1-F64L-S65T-GFP fusion
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Best Local Similarity 61.1%;
Matches 601; Conservative
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US-09-417-197-56
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NAME/KEY: CDS
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318 IGITCAGGACCICAIGGAGACGGACCI---GIACAAGCICCIAAAAGAGCCAGCAGCIGAG 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       258 CATAGGCATCCGAGACATCCTCAGAGCACCCACCCTGGAAGCCATGAGAGATGTTTACAT 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1747;
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22.8%; Score 318; DB 2; Length 174
Best Local Similarity 60.1%; Pred. No. 1.9e-60;
Matches 591; Conservative 0; Mismatches 375; Indels
                           APPLICANT: Panayotatos, Nikos
TITLE OF INVENTION: A Family of Map2 Protein Kinases
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,620A
FILING DATE: 03-JAN-1994
CLASSIFICATION: 800
ATTONEX/AGENT INFORMATION:
NAME: MISROCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-123
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
                                                                                                                                                                ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1747 harr
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                               CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d:
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STRANDEDNESS: single
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US-08-176-620A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              464 AGGCGGTATATCAAGCACCTGCCTCGACAGTCGCCTATTCCCTTAACCCAGAAGTTCAGA 405
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                                                                                                                                                                                                                                                                     Length 953;
                                                                                                                                                                                                                                                                     Score 319.8; DB 3; Length
Pred. No. 6.3e-61;
0; Mismatches 267; Indels
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Cobb, Melanie H.
Yancopoulos, George D.
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Patent No. 5595904
GENERAL INFORMATION:
APPLICANT: Boulton, Teri G.
APPLICANT: Cobb, Melanie H.
APPLICANT: Yancopoulos, George D.
                                                                                                                                    ) TYPE: DNA
; ORGANISM: Physcomitrella patens
US-09-828-313-8
                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 64.7%;
Matches 491; Conservative
NUMBER OF SEQ ID NOS: 128
SOFTWARE: Patentin Ver. 2.
SEQ ID NO 8
LENGTH: 953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
US-08-176-620A-1
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22.8%; Score 318; DB 2; Length 17.
Best Local Similarity 60.1%; Pred. No. 1.9e-60;
Matches 591; Conservative 0; Mismatches 375; Indels
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1747 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                               TYPE: nucleic acid
STRANDENDESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
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; LOCATION:
US-08-463-862-1
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                           CCTTAAGATCTGTGATTTTGGCCTTGCCCGGATTGCTGACCCTGAGCACGACCACTGG
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                                                                                                                                                                                   CACCGACTACTCCGCCGCCATCGACGTCTGGTCCGTCGGCTGCATCTTCATGGAGCTCAT
                                                                            1035 GCTGAAGGAGCTGATCTTCCAAGA 1058
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REGISTRATION NUMBER: 18,872
REPERBENCE/DOCKET NUMBER: 6526-049
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
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US-08-463-862-1
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1070 GCCCATCTGCCTGGAGCCCTTCTTCGACTTCGAGCAGAAGGCTCTAAACGAGGACCA 1129
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CTTTGAGACGAGGAGATGGTGGCGATAAAGAAGATCGCCAACGCGTTCAACAACGACAT 301
                                 CCACGTGCGCAAGACCAGAGTGGCTATCAAGAAGAT---CAGCCCCTTCGAGCATCAAAC 197
                                                                                                                                                                                                                                                                                                                                                                 302 GGACGCCAAGCGCACGCTCCGGGAGATCAAGCTCCTCAGGCACCTCGACCACGAGAACAT
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A PAMILY OF MAP2 PROTEIN KINASES
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Patent No. 5914261
GENERAL INFORMATION:
APPLICANT: Boulton, Teri G. et
TITLE OF INVENTION: A FAMILY OF
NUMBER OF SEQUENCES: 11
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US-08-458-887-1
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Pred. No. 1.9e-60;
0; Mismatches 375; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Boulton, Teri G.
APPLICANT: Cobb, Melanie H.
APPLICANT: Yancopoulos, George D.
APPLICANT: Nye, Steven
APPLICANT: Panayotatos, Nikos
APPLICANT: Panayotatos, Nikos
NITIE OF INVENTION: A Family of Map2 Protein Kinases
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE PATENTIA FOLSONIA #1.25
SOFTWARE PATENTIA FALE
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,985
FILING DATE: 05-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/176,620
FILING DATE: 03-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                 1035 GCTGAAGGAGCTGATCTTCCAAGA 1058
                                                                                                                                                                                          1130 AATGAAGCAGCTGATCTTCAACGA 1153
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REGISTRATION NUMBER: 18, 872
REFERENCE/DOCKET NUMBER: 6526-123
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTY: 0.52.F.

ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (212) 790-9090
TELERA: (212) 869-8864/9741
TELEX: 66141 PENNIE
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1747 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08461985
Patent No. 5872006
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MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 60.1
Matches 591; Conservative
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ADDRESSER: Pennie &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1..1095
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US-08-461-985-1
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US-08-461-985-1
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GENERAL INFORMATION:

APPLICANT: Boulton et al.

TITLE OF INVENTION: ANTIBODIES DIRECTED TOWARD EXTRACELLULAR SIGNAL-RELATED

TITLE OF INVENTION: ANTIBODIES DIRECTED TOWARD EXTRACELLULAR SIGNAL-RELATED

TITLE OF INVENTION: KINASES

FILE REFERENCE: REG 430-A-1

CURRENT APPLICATION NUMBER: US/08/932,787B

PRIOR APPLICATION NUMBER: 08/469,547

PRIOR FILING DATE: 1997-00-18

PRIOR FILING DATE: 1994-01-07

PRIOR FILING DATE: 1994-01-07

PRIOR PILING DATE: 1994-01-07

PRIOR APPLICATION NUMBER: 07/701,544

PRIOR APPLICATION NUMBER: 07/532,004

PRIOR FILING DATE: 1990-06-01

NUMBER OF SEQ ID NOS: 21

SEQ ID NOS: 21

SEQ ID NOS: 21

SEQ ID NOS: 21

SEQ ID NOS: 21

SEQ ID NOS: 21

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SEQ ID NOS: 21
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                                                                                                            CAACCGCCAGCCGCTCTTCCCCCGGCAGGGACCACATGCACCAGATGCGCCTCATCACCGA
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CCTTAAGATCTGTGATTTTGGCCTTGCCCGGATTGCTGACCCTGAGCACGACCACACTGG
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US-08-932-787B-1
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US-08-932-787B-1
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Pred. No. 1.9e-60;
0; Mismatches 375; Indels 18; Gaps
                       COURTY: New York
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READELF FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,887
FILING DATE: 02-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/458,887
FILING DATE: 02-JUN-1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/458,887
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
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MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 60.1%;
Matches 591; Conservative
      CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie &
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          APPLICANT: BOULTON et al.

TITLE OP INVENTION: A FAMILY OF MAP2 PROTEIN KIN.
FILE REFERENCE: REG 430-Y-1
CURRENT APPLICATION NUMBER: US/08/932,012C
CURRENT FILING DATE: 1997-09-17
PRIOR PLING DATE: 1995-06-05
PRIOR PLING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: 08/178,488
PRIOR PLING DATE: 1995-01-07
PRIOR APPLICATION NUMBER: 07/701,544
PRIOR PLING DATE: 1991-05-16
PRIOR PLING DATE: 1990-06-01
NUMBER OF SEQ ID NOS: 21
SOPTWARE: FRASESQ for Windows Version 3.0
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THER INFORMATION: ERK1 CDNA
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Best Local Similarity
Matches 591; Conserva'
                                                                                                                                                                                                                                                                                                                   ORGANISM: RAT
                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
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  CATAGGCATCAGGGATGTGATCCCGCCGCCGATCCCTCAGGCGTTCAACGACGTCTACAT
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TITLE OF INVENTION: A PAMILY OF MAP2 PROTEIN KINASES
FILE REFERENCE: REG 430-V-1
CURRENT APPLICATION NUMBER: US/08/88,818C
CURRENT FILING DATE: 1997-07-07
PRIOR PILING DATE: 1995-06-07
PRIOR PILING DATE: 1995-06-07
PRIOR PILING DATE: 1994-01-07
PRIOR PILING DATE: 1994-01-07
PRIOR PILING DATE: 1994-01-07
PRIOR PAPLICATION NUMBER: 07/701,544
PRIOR PILING DATE: 1994-01-07
PRIOR PILING DATE: 1990-06-01
PRIOR PILING DATE: 1990-06-01
SEQ ID NOS: 21
SOFTWARE: PREUSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1747
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Patent No. 6303358
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OTHER INFORMATION: ERK1 CDNA
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166033,
166036,
5422, Ap
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                                                                          December 29, 2005, 05:07:08; Search time 839 Seconds (without alignments) 13759.299 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

3: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

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7: /cgn2_6/ptodata/1/pubpna/USOB_PUBCOMB.seq:*

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9: /cgn2_6/ptodata/1/pubpna/USOB_PUBCOMB.seq:*

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           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-425-114-22843

US-10-425-114-28439

US-10-425-118-86951

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Maximum Match 100%
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US-10-768-886-1

Sequence 1, Application US/10768886

Publication No. US20040209325A1

GENERAL INFORMATION:

APPLICANT: Board of Trustees for University of Arkansas

TITLE OF INVENTION: Mitogen-Activated Protein Kinase and Method of UNIVERTION: Mitogen-Activated Protein Kinase and Method of TITLE OF INVENTION: Biotic and Abiotic Stress Tolerance in Plants

FILE REFERENCE: UAF-03-14

CURRENT APPLICATION NUMBER: US/10/768,886

CURRENT FILING DATE: 2004-01-31

NUMBER OF SEQ ID NOS: 8

SEQ ID NO: 3.2

SEQ ID NO: 3.2
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Conservative 0; Mismatches
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ORGANISM: Oryza sativa
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Best Local Similarity
Matches 1396; Conser
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Best Local Similarity 82.9 Matches 1051; Conservative
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Sequence 14213, Application US/10767701

Sublication No. US20040172684A1

GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwel
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701

NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 14213
LENGTH: 1610
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US-10-767-701-14213
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82.9%; Pred. No. 9.5e-254;
iive 0; Mismatches 206;
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                                    249 GATGACGCACGGCGCCGCTTCCTCCTCTACAACATATTCGGCAACCAGTTCGAGATCAC
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US-10-425-115-6734

Sequence 6734, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21 (53222) B
CURRENT PILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 6734
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POGANISM: Zea mays
POGATURE:
OTHER INFORMATION: Clone ID: MRT4577_106134C.1
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Best Local Similarity 82.0<sup>1</sup>
Matches 1005, Conservative
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Sequence 5013, Application US/10739930
Publication No. US20040216190A1
GENERAL INFORMATION:
GENERAL INFORMATION:
FAPLICATION:
TITLE OF INVENTION:
PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
TITLE OF INVENTION:
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TITLE OF INVENTION:
PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
TITLE OF INVENTION:
TOTAL OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 44.6%; Score 623.2; DB 8; Best Local Similarity 70.9%; Pred. No. 5.9e-171; Matches 892; Conservative 0; Mismatches 343;
                                                                                                                                                                                                                                                    1367 GAACTITGGATTAAAAAAAAAAAAAAA 1396
                                                                                                                                                                                                                                                                                               GAACTTTGGATTAAAAAAAAAAAAAAAA 1084
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US-10-739-930-5013
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                                                                                                                                                                                                                                             Sequence 3, Application US/10768886
Publication No. US20040209325A1
GENERAL INFORMATION: US20040209325A1
GENERAL INFORMATION: US20040209325A1
APPLICANT: Board of Trustees for University of Arkansas
TITLE OF INVENTION: Mitogen-Activated Protein Kinase and Method of Use to Enhance
TITLE OF INVENTION: Mitogen-Activated Protein Kinase and Method of Use to Enhance
TITLE OF INVENTION: Mitogen-Activated Protein Kinase and Method of Use to Enhance
TITLE OF INVENTION: MAPPLICATION NUMBER: US/10/768,886
CURRENT FILING DATE: 2004-01-31
NUMBER OF SEQ ID NOS: 8
SOPTWARE: PatentIn version 3.2
                          GGTGCAGCCCGCCGCGCTCGACCTCATCGAGAGGATGCTCACCTTCAACCCGCTGCAGAG 1006
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GCAGAAGGCTCTAAACGAGGACCAAATGAAGCAGCTGATCTTCAACGAAGCGATCGAGAT
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Pred. No. 3.5e-225;
0; Mismatches 1;
                                                                                                                  CAACCCCAGTTTCCGATATTAGCTAG 1414
                                                                                       1166 GAACCCAAACATCCGGTACTAGATTG 1191
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Best Local Similarity 99.9%;
Matches 809; Conservative
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US-10-768-886-3
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; FEATURE:
; OTHER INFORMATION: Clone ID: 700242603_FLI
US-10-425-114-3164
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Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: APPLICANT: Screen, Steven B

APPLICANT: Screen, Steven B

APPLICANT: Tabask, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: NUMBER: US/10/425,114

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT PILING DATE: 2003-04-28

SEQ ID NO 3164

LENGTH: 873
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APPLICANT: Kreps, Joeff
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APPLICANT: Kreps, Joef
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE REPERENCE: SCRIPING NOWBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
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           Length 873
                                                                                                                Indels
                                                                                                                                                                                                                           CACTCGGCGAACGTGATCCACCGCGACCTGAAGCCGAGCAACC
Score 543; DB 7; 1
Pred. No. 1.2e-147;
                                                                                                                0; Mismatches
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Query Match
Best Local Similarity 89.3%;
Matches 585; Conservative
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US-09-938-842A-644
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TRANSGENIC PLANTS CONTAINING
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                                   GCACGACATCGCCGATGAGCCCATCTGCCTGGAGCCCTTCTCCTTCGACTTCGAGCAGAA
                                                                                                         GGCTCTAAACGAGGACCAAATGAAGCAGCTGATCTTCAACGAAGCGATCGAGATGAACCC
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Pred. No. 1.3e-137;
0; Mismatches 357;
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Sequence 644, Application US/09938842A

Publication No. US20040009476A9

GENERAL INFORMATION

APPLICANT: HARDER, Joel

APPLICANT: Wang, Xun

APPLICANT: Zhu, Tong

TITLE OF INVENTION: SARE, AND METHODS OF PLAN

TITLE OF INVENTION: SARE, AND METHODS OF USE

TITLE OF INVENTION UNBER: US/09/938,842A

CURRENT FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: US 60/264,647

PRIOR APPLICATION NUMBER: US 60/264,647

PRIOR APPLICATION NUMBER: US 60/20,111

PRIOR PILING DATE: 2001-01-16

PRIOR PILING DATE: 2001-06-22

NUMBER: OF SEQ ID NOS: 5379
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Best Local Similarity 67.2%;
Matches 736; Conservative
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                                                                                                                                                           3;
                                                                                                                          Length 1188;
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                                                                                                                      Score 508.8; DB 3;
Pred. No. 1.3e-137;
0; Mismatches 357;
                                                 ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-644
                                                                                                                      Query Match
Best Local Similarity 67.2%;
Matches 736; Conservative
5379
NUMBER OF SEQ ID NOS:
                                   1188
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                                                                                    TACGACATCTTCGGGAACAAGTTCGAGGTGACGAACAAGTACCAGCCGCCCATCATGCCC
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                            Length 1637;
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                           Score 492.2; DB 7;
Pred. No. 1.1e-132;
                                                       0; Mismatches 388;
                           35.3%;
                                                       725; Conservative
                                          Similarity
JS-10-425-114-22355
                         Query Match
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Matches 725
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US-10-425-114-22355

Sequence 22355, Application US/10425114

Publication No. US20040034888A1

GENERAL INPORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Screen, Steven E

APPLICANT: Screen, Steven E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313)B

CURRENT APPLICANTON NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 22355

LENGTH. 16-77
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                                                                         GAGCAACCTGCTGAACGCCAACTGCGACCTCAAGAT
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OTHER INFORMATION: Clone ID: LIB3476-029-E9_FLI
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ORGANISM: Sorghum bicolor
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; Sequence 28439, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
    APPLICANT: Liu, Jinddong
; APPLICANT: Liu, Jinddong
; APPLICANT: Zhou, Yihua
    APPLICANT: Screen, Steven E
    APPLICANT: Cao, Yongwei
; APPLICANT: Cao, Yongwei
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REPERENCE: 38-21 (5313) B
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 28439
LENGTH: 1520
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TACCGCGCGCGGAGCTGCTGCTCAACTCCAACTACTACTCCGCCGCCATCGACGTCTGG
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64.8%; Pred. No. 7.8e-131;
tive 0; Mismatches 392;
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US-10-425-114-28439
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Best Local Similarity
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                                                                                                                                                                                                                               Sequence 14217, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Covalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Covalic, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION UMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
                      TTCGAGCAGAAGGCTCTAAACGAGGACCAAATGAAGCAGCTGATCTTCAACGAAGCGATC 1160
                                                          1241 TTTGAĞCAACCATCCTTTACAGAĞCGCATATAAAAGAACTTATCTGGAGGAATCTTTA 1300
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US-10-767-701-14217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 492.2; DB 7;
Pred. No. 1.1e-132;
0; Mismatches 388;
                                                                                                 1161 GAGATGAACCCAAACATCCGGTACTAGATTGAA 1193
                                                                                                                                   1301 GCATÍTAACCCGGATCCTCCCTACTAATTTCAA 1333
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Best Local Similarity 65.1%;
Matches 725; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Sorghum bicolor
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US-10-767-701-14217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 14217
LENGTH: 1707
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Query Match 34.8%;
Best Local Similarity 64.8%;
Matches 721; Conservative
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ORGANISM: Zea mays
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                                          ATTGGCCGCGCGCCTACGGGATCGTCTGCTCCGTGATGAACTTTGAGACGAGGGAGATG
                                                                                                  218 GTTGCGATCAAGAAGGTTGGCATTCGACAACCACATCGACGCCAAGCGGACGCTC
                                                                                                                                  CGGGAGATCAAGCTCCTCAGGCACCTCGACCACGAGAACATCATAGGCATCAGGGATGTG
                                                                                                                                                                              381 ATCCCGCCGCTCACTCCTCAGGCGTTCAACGACGTCTACATCGCCACGGAGCTCATGGAC
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Sequence 86951, Application US/10425115

Sequence 86951, Application US/10425115

Publication No. US20040214272A1

SEQUENCE 86951, Application No. US20040214272A1

SEQUENCE 86951, Application No. US20040214272A1

APPLICANT: La Rosa, Thomas J.

APPLICANT: Applicant: No. Vinua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(53222)B

CURRENT APPLICANTION NUMBER: US/10/425,115

CURRENT PILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NOS: 369326

FENCENTION NUMBER OF SEQ ID NOS: 369326 ö 1524 GGCGGCGGCGGTGGAGCGCAGATCAAGGGTATGGCGACGCACGGGGGCCCCCTACGTGCTG 1465 1224 ATTCGGCCCCCAACTAGAGAACTTTAATGACGTGTACATTGTTACTGAGTTAATGGAT 1165 140 620 985 740 925 261 GTGGCGATAAAGAAGATCGCCAACGCTTCAACAACGACATGGACGCCAAGCGCACGCTC 321 CGGGAGATCAAGCTCCTCGACCTCGACCACGAGAACATCATAGGCATCAGGGATGTG ATCCCGCCGCCGATCCCTCAGGCGTTCAACGACGTCTACATCGCCACGGAGCTCATGGAC 984 GGGCTTGCAAGGACCACTTCAGAGACAGATCTCATGACAGAGTATGTGGTCACTGGTCACTTGG TACCGCGCGCCGGAGCTGCTGCTCAACTCCACCGACTACTCCGCCGCCATCGACGTCTGG 201 ATTGGCCGCGCGCCCTACGGGATCGTCTGCTCCGTGATGAACTTTGAGACGAGGGAGATG ACCGACCTCCATCACATCATCCGCTCCGAACCAAGAACTGTCAGAAGAGCACTGCCAGTAT 1044 GATCTGAAGCCGAGCAATTTGTTCCTAAATGCAAATTGTGACCTCAAGATTGCAGACTTT GGGCTGGCGCCGCCGTCGTCGGAGAGCGACATGATGACGGAGTACGTGGTCACCCCGGTGG 924 TACCGGGCACCAGAGCTGCTGTTGAACTGTTCACAGTATACTGCTGCTGCTATTGATGTCTGG 81 GACGGGCGCCCGGTGCCGGAGTTCAGGCCGACGATGACGCACGGCGCCGGTACCTGCTC 141 TACGACATCTTCGGGAACAAGTTCGAGGTGACGAACAAGTACCAGCCGCCCATCATGCCC 1464 TACAACGIGIACGGAAACCICTICGAGGICTCCTCCAAGTACGCCCCACCAACTCCGCCCC TTCCTGTACCAGATCCTGCGGGGGCTCAAGTACATCCACTCGGCGAACGTGATCCACCGC GACCTGAAGCCGAGCAACCTGCTGAACGCCAACTGCGACCTCAAGATCTGCGACTTC ö Length 1803; Indels Score 485.8; DB 8; Pred. No. 8.4e-131; 0; Mismatches 392; , OTHER INFORMATION: Clone ID: MRT4577_179305C.1 US-10-425-115-86951 741 ð

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10-10-425-114-6328
1 Sequence 6328, Application US/10425114
2 Publication No. US20040034888A1
3 GENERAL INFORMATION:
3 APPLICANT: Liu, Jingdong
3 APPLICANT: Zhou, Yihua
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Fublication No. US20040123343A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Bunkharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53221)8
CURRENT APPLICANT: 2003-05-14
NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 36761

LENGTH: 1717
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                                                                                        684 CAGGACTTCCGCCTGCGTTTCCGCAACATGTCTCCTGGCGCAGTCGATTTGTTGGAAAGG
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, OTHER INFORMATION: Clone ID: PAT_MRT4530_40555C.1
US-10-437-963-36761

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US-10-437-963-36761/C
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RESULT 15

US-10-424-599-141942

US-10-424-599-141942, Application US/10424599

; Sequence 141942, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J

; APPLICANT: La Rosa Thomas J

; APPLICANT: Cao Yongwel

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 141942
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     663 GCTCGCTGTTGAATACCGAGACGAATGAGCTGGCGGGTTAAGAAGATAGCGATT
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                                                                                                                                                           1434 TIACAGTIGAAGAAGCACTAGCCCATCCATACCTIGAAAAACTGCATGAAGTAGCTGATG
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Pred. No. 1.6e-125;
0; Mismatches 297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Clone ID: PAT_MRT3847_99188C.1
US-10-424-599-141942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 68.5%;
Matches 646; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Glycine max
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APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E.

APPLICANT: Tabaeka, Jack E.

APPLICANT: Tabaeka, Jack E.

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associat

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF PRERENEUR: 38-21(53313) B.

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT PILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

FER ID NO 6328
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33.5%; Score 467.8; DB 7;
Best Local Similarity 68.5%; Pred. No. 1.6e-125;
Matches 646; Conservative 0; Mismatches 297;
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US-10-425-114-6328
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           949 TGCAGCCCGCCCCGCGCTCGACCTCATCGAGAGGATGCTCCACCTTCAACCCGCTGCAGAGAA 1008
                                                                                                                                                     1383 TTCATCCGGCAGCCATTGATGATGTTGAAAAATGTTGACAGTTGATCCCACCAAAAAA 1442
                                                                                                                                                                            1009 TCACAGTTGAGGAGGCGCTCGATCATCCTTACCTAGAGAGATTGCACGACATCGCCGGTG 1068
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Sequence 28925, A
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Sequence 37, Appl
Sequence 35100, A
                                                                         December 29, 2005, 05:17:30 ; Search time 195 Seconds (without alignments) 3752.939 Million cell updates/sec
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                                                                                                                                                                                                          4172979 segs, 262114271 residues
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Maximum Match 100%
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Maximum DB seq length: 200000000
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Sequence 21, Appl
Sequence 367, Appl
Sequence 1, Appli
Sequence 99, Appli
Sequence 54380, A
Sequence 15, Appli
Sequence 11, Appli
Sequence 1, Appli
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Sequence 1, Appli
Sequence 38025, A
Sequence 138, Appli
Sequence 37, Appli
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37, Appl
17, Appl
52966, A
11, Appl
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Sequence 2, Appli
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Sequence 176, P
Sequence 142, P
        Sequence 1,
Sequence 6,
Sequence 21
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Sequence
Sequence
US-10-966-483-1

US-10-981-029-6

US-10-981-234-367

US-10-821-234-367

US-10-821-234-99

US-10-821-234-99

US-10-921-234-99

US-10-950-185-54380

US-11-079-691-15

US-10-750-185-58025

US-10-750-185-58025

US-10-750-185-52966

US-10-770-726-37

US-10-770-726-37

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US-11-005-029-11

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ALIGNMENTS

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182 CCAGCCGCCCATCATGCCCATTGGCCGCGCGCCTACGGGATCGTCTGCTCCGTGATGAA 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                carcescarcesadacarrerseceserencesecereseaseceareasadarereradar 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cracacecaerrecaeracarcesceaesescecaracecaresrcaecresescrarea 254
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| Sequence 5. Application No. US20050266420A1 |
| Publication No. US20050266420A1 |
| GENERAL INFORMATION: |
| APPLICANT: PUSZTA, LAJOS |
| APPLICANT: STEC, JAMES |
| APPLICANT: AYERS, MARK |
| APPLICANT: STEC, JAMES |
| TITLE OF INVENTION: MULTIGENE PREDICTORS OF RESPONSE TO CHEMOTHERAPY |
| TITLE OF INVENTION: MULTIGENE PREDICTORS OF RESPONSE TO CHEMOTHERAPY |
| TITLE OF INVENTION: MULTIGENE PREDICTORS OF RESPONSE TO CHEMOTHERAPY |
| TITLE OF INVENTION: MULTIGENE PREDICTORS OF RESPONSE TO CHEMOTHERAPY |
| TITLE OF INVENTION NUMBER: US/10/955,054A |
| CURRENT FILING DATE: 2004-09-30 |
| NUMBER OF SEQ ID NOS: 195 |
| SEQ ID NO 5 |
| LENGTH: 1866 |
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| LENGTH: 1866 |
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Best Local Similarity 61.3
Matches 603; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
CORGANISM: Homo sapiens
US-10-955-054A-5
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149 CTTGGGGAACAAGTTGGAGGTGACGAACAAGTACCACCACCACCATGGCGGAACAACAAGAACTACGGAACATTCGGCGAACACCCCACTGGGAACATTCGGCGAACACCCCACTGGGAACATTCGGCGAACACCCCCACACGGAACACCCCCACACGGAACACCCCCACACGGAACACCCCCACACGGAACACCCCCC	1145 CAGCCCCATTGCCCGGAA 1162
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THE CAGTATTTCCTGTACCAGATCCTGCGGGGGCTCAA ANTICTGCTACTTCCTCTACCAGATCCTGCGGGGGCTCAA SATCCACCGCGACCTGAAGCCGTCGCGGGGCCTCAACCTGCTGAAGCCCTCACCTGCTCGCGGGCCTCGGCGGGGCTTCGCTCGC	Query Macch 20.0%; Score 278.8; DB 6; Length 1888; Best Local Similarity 56.5%; Pred. No. 1.7e-54; Matches 586; Conservative 0; Mismatches 437; Indels 15; Gaps 3;

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APPLICANT: Jain, Ravi
APPLICANT: Bhat, Balkrishen
APPLICANT: Bhat, Balkrishen
APPLICANT: Brail Ravi
APPLICANT: Brail Rigen
ITILE OF INVENTION: Oligomeric Compounds And Compositions For Use In Modulation
ITILE OF INVENTION: Of Small Non-Coding RNAs
FILE REPERENCE: ISISOBO-100 (COREOUGUS)
CURRENT APPLICATION NUMBER: US/10/909,125
CURRENT APPLICATION NUMBER: US 60/492,056
PRIOR PILING DATE: 2003-07-31
PRIOR PILING DATE: 2003-07-31
PRIOR APPLICATION NUMBER: US 60/516,303
PRIOR PILING DATE: 2003-10-31
PRIOR FILING DATE: 2003-10-31
PRIOR FILING DATE: 2004-04-14
NUMBER: OF SEQ ID NOS: 2184
SEQ ID NO 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1019 GGAGGCGCTCGATCATCCTTACCTAGAGATTGCACGACATCGCCGATGAGCCCCATCTG 1078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGAAGCACCATTCAAGTTCGACATGGAATTGGATGACTTGCCTAAGGAAAAGCTAAAAGA 1361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1122 TTCTCTTCCACACAAAAAAAGGGCCCATGGAACAGGCTGTTCCCAAATGCTGACTCCAA 1181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       899 GCACCTGCCGCAGTACCCGCGCCGGACGTTCGCGAGCATGTTCCCGGGGTGCAGCCCGGC 958
                                                                                                                                                                    719 CTCCGCCGCCATCGACGTCTGGTCCGTCGCTGCATCTTCATGGAGCTCATCAACCGCCA 778
822 CTGTGACTTTGGCCTGGCCCGTGTTGCAGATCCAGACCATGATCACACAGGGTTCCTGAC 881
                                                                                                                                                                                                                                                                                                                                         1002 GCCCATCTTTCCAGGAAGCATTATCTTGACCAGCTGAATCACATTTTGGGTATTCTTGG
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                                                                                                              882 AGAATATGTGGCCACACGTTGGTACAGGGCTCCAGAAATTATGTTGAATTTCCAAGGGCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Baau, Christine
APPLICANT: Lollo, Bridget
APPLICANT: Bennett, C. Frank
APPLICANT: Freier, Susan M.
APPLICANT: Griffey, Richard H.
APPLICANT: Baker, Brenda F.
APPLICANT: Vickers, Timochy
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Koller, Erich
Swayze, Eric
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APPLICANT: Guillemette, Tracy L.
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Kanatkar, Shubhangi
APPLICANT: Kanatkar, Shubhangi
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Thibodeau, Stephen N.
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, METHODS FOR IDENTIFICATION, ASSESSMENT, FREVENTION, TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, FILLE REFERENCE: MPMOI-029P2RNM
CURRENT TRIING DATE: 2005-07-21
PRIOR PILLING DATE: 2002-11-21
PRIOR FILLING DATE: 2001-11-21
PRIOR PELICATION NUMBER: US 60/361,978
PRIOR PILLING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          191 CATCATGCCCATTGGCCGCGCGCCTACGGGATCGTCTGCTCCGTGATGAACTTTGAGAC 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         251 GAGGGAGATGGTGGCGATAAAGAAGATCGCCAACGCGTTCAACAACGACATGGACGCCAA 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCTCATGGACACCGCCTCCATCACATCACCGCTCCAAGAACTGTCAGAAGAGA
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                                                                                   Sequence 114, Application US/11186284
Publication No. US20050266493A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 55.7
Matches 564; Conservative
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                                                                                                                                                                                                                                                                                                                                          Query Match 11.6%; Score 161.4; DB 6; Best Local Similarity 51.4%; Pred. No. 1.1e-27; Matches 428; Conservative 0; Mismatches 396;
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: Patentin version 3.2
SEQ ID NO 5
                                                                                                                                                                                                         TYPE: DNA ORGANISM: Homo sapiens
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                                                                                                                                                                          Length 2737;
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                                                                                                                                                                       Score 234; DB 6; Lo
Pred. No. 3.1e-44;
0; Mismatches 300;
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; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM101079 (031896-010000)
                                                                                                                                                                          16.8%;
58.2%;
                                                                                                                                                                   Query Match
Best Local Similarity 58.2
Matches 439; Conservative
                                                              , ORGANISM: H. sapiens
US-10-909-125-861
      LENGTH: 2737
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Sequence 28, Application US/1077026
Publication No. US20050266409A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING, TITLE OF INVENTION: CANCERS
FILE REFERENCE: AMI01079 (031896-010000)
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT APPLICATION NUMBER: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: Patentin version 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 135.4; DB 6; Length 3 Pred. No. 9.9e-22; 0; Mismatches 401; Indels
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Best Local Similarity 50.9
Matches 437; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
US-10-770-726-28
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                                                                                          APPLICANT: BRAUN, ANDREAS
APPLICANT: BRAUN, ANDREAS
APPLICANT: BRAUN, MATHEW ROBERTS
APPLICANT: RENELAND, MATHEW ROBERTS
APPLICANT: RENELAND, RIKARD HENRY
APPLICANT: RENELAND, RIKARD HENRY
APPLICANT: RENELAND, RIKARD HENRY
APPLICANT: HOYAL-WRIGHTSON, CAROLYN R.
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION WHORER: US/10/857,780
CURRENT APPLICATION NUMBER: US/10/34
FRIOR FILING DATE: 2003-11-25
FRIOR APPLICATION NUMBER: 60/490,234
FRIOR FILING DATE: 2003-11-25
FRIOR APPLICATION NUMBER: 60/525,239
FRIOR FILING DATE: 2003-11-25
NUMBER OF SEQ ID NOS: 4962
SOFTWARE PATENTIN VERSION 3.2
SEQ ID NO 11
LENGTH: 2372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              713 CGACTACTCCGCCGCCATCGACGTCTGGTCGGCTGCATCTTCATGGAGCTCATCAA 772
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Pred. No. 4.8e-23;
0; Mismatches 350;
   Sequence 11, Application US/10857780 Publication No. US20050272043A1 GENERAL INFORMATION:
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Best Local Similarity 52.7%;
Matches 406; Conservative
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Sequence 7, Application US/1077076

Publication No. US20050266409A1

GENERAL INFORMATION:

APPLICANT: Weath

APPLICANT: Liu, Wet

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING

TITLE OF INVENTION: CANCERS.

TITLE OF INVENTION: CANCERS.

FILE REFERENCE: AMI/10/79 (031896-010000)

CURRENT APPLICATION NUMBER: US/10/770,726

CURRENT PILING DATE: 2004-02-04

NUMBER OF SEQ ID NOS: 48640

SOFTWARE: PATENTIN Version 3.2

SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  975 GAGAGGATGCTCACCTTCAACCCGCTGCAGAGAATCACAGTTGAGGAGGCGCTCGATCAT 1034
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                    GACCTGAAGCCGAGCAACCTGCTGAACGCCAACTGCGACCTCCAAGATCTGCGACTTC
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                                                   GACCTGAAGCCCCAGAACCTGCTAATAAACAGGAATGGGGAGCTGAAATTGGCTGATTTT
                                                                                                       GGGCTGGCGCCGTCGTCGGAGAGCGACATGA----TGACGGAGTACGTGGTCACCCGG
                                                                                                                                                  460 GGCCTGGCTCGAGCCTTTGGGATTCCCGTCCGCTGTTACTCAGCTGAGGTGGTCACAGG
                                                                                                                                                                                                                                                                              738 IGGICCGICGCTGCATCTTCATGGAGCTCATCAACC---GCCAGCCGCTCTTCCCCGGC
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CORGANISM: Homo sapiens
US-10-770-726-7
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US-10-770-726-7
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Publication US/2050266409A1
Sequence 9, Application US/1077026
Publication No. US20050266409A1
SEQUENCE INFORMATION:
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
TITLE OF INVENTION: CANCERS
FILE REFERENCE AMIO1079 (031896-010000)
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: Patentin version 3.2
SEQ ID NO 9
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50.6%; Pred. No. 3.4e-20;
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Matches 429; Conservative
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Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MAI GENOMICS, INC.
APPLICANT: RERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: ROSENFELD, David
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MAII100-2
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Pred. No. 1.2e-12;
0; Mismatches 299; Indels
PRIOR APPLICATION NUMBER: 60/322,358
PRIOR PILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: 60/294,075
PRIOR PILING DATE: 2001-05-29
PRIOR FILING DATE: 2001-05-29
PRIOR PILING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 190
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 11
LENGTH: 3073
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48.8%;
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Best Local Similarity 48.8
Matches 288; Conservative
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US-11-113-424-11
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Sequence 11, Application US/11113424

Publication No. USCOSCOSCO0713A1

APPLICANT Gangolli et al.

TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same

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TURRENT FILLAGO DATE: 2005-04-21

PRIOR PPLING DATE: 2005-04-21

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PRIOR PPLING DATE: 2000-12-19

PRIOR APPLICATION NUMBER: 60/257, 314

PRIOR PPLING DATE: 2000-12-20

PRIOR APPLICATION NUMBER: 60/311, 613

PRIOR PLING DATE: 2010-08-10

PRIOR PPLING DATE: 2010-08-10

PRIOR PPLING DATE: 2010-08-10

PRIOR PLING DATE: 2010-08-10
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Sequence 27, Application US/1077026
Publication No. US20050266409A1
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GUNERAL FILING BATE:
GOFTWARE:
FRIENCE OF SEQ ID NOS: 48640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1400;
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Best Local Similarity 56.9%; Pred. No. 6.2e-12;
Matches 189; Conservative 0; Mismatches 140; Indels
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Publication No. US2005026409A1
GENERAL INPORMATION:
APPLICANT: Wyeth
APPLICANT: Liu, Wei
TITLE OF INVENTION: CAMPOSITIONS AND METHODS FOR:
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AM101079 (031896-010000)
CURRENT PAPLICATION NUMBER: US/10/770,726
CURRENT FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
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CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR PILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 28925
LENGTH: 1400
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US-10-750-185-28925
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Best Local Similarity
Matches 201; Conserv
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US-10-770-726-8
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1484 ACAACCTCCTGCACCAGCAGATGCTGCAGTCGGAGATCCAGGCCATGAAGAAGCTGCGGC 1543
                                                                                                            1544 ACAAACACATCCTGGCGCTGTACGCCGTGGTGCGGGGGGGCCCCGTGTACATCATCA 1603
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                                                       352 ACGAGAACATCATAGGCATCAGGGATGTGATCCCGCCGCCGATCCCTCAGGCGTTCAACG 411
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Sequence 35, Application US/1077026
Publication No. US200506409A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Brown, Eugene
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AM101079 (031896-010000)
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: Patentin version 3.2
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46.9%; Pred. No. 0.00013;
tive 0; Mismatches 251; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 4.5%; Score 63; DB 6; Length 2497; Best Local Similarity 65.0%; Pred. No. 3e-05; Matches 93; Conservative 0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                 APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: PANTIN, Dennis
FILLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR PPLICATION NUMBER: US 60/437,482
PRIOR PILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
  1726 ATTGAGATGGTGGACGGAGAGCCCCCTAC 1755
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                                                                                                                                Sequence 35100, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
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; ORGANISM: Bovine 19866881358776
US-10-750-185-35100
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SEQ ID NO 35100
LENGTH: 2497
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Best Local Similarity 46.9
Matches 227; Conservative
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Sequence 134,
Sequence 115
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2: /cgn2 6/ptodata/2/pubpaa/US06 NEW PUB.pep:*
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8: /cgn2 6/ptodata/2/pubpaa/US10 NEW PUB.pep:*
8: /cgn2 6/ptodata/2/pubpaa/US11 NEW PUB.pep:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-11-1109-1239-4
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Maximum Match 100%
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APPLICANT: Thibodeau, Stephen N.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Thibodeau, Stephen N.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: THERAPY OF COLON CANCER
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REPRESENCE: MPMO1-029PZRM
CURRENT APPLICATION NUMBER: US/11/186,284
CURRENT APPLICATION NUMBER: US/10/301,822
PRIOR APPLICATION NUMBER: US/10/301,822
PRIOR PILING DATE: 2002-11-21
PRIOR PILING DATE: 2002-11-21
PRIOR PILING DATE: 2002-12-10
PRIOR PILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,978
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR PILING DATE: 2002-03-05
PRIOR PILING DATE: 2002-05-20
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                                         LERLHDIADEPICLEPFSFDFEQKALNEDQMKQLIFNEAIEMNPNIR 367
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                      LERLHDIADEPICLEPFSFDFEQKALNEDQMKQLIFNEAIEMNPNIR
                                                                                                                                                                   Sequence 115, Application US/11186284
Publication No. US20050266493A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 115
                                                                                                                                                                                                                 APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Samatkar, Shubhangi,
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Thibodeau, Stepher Trees
APPLICANT: Thibodeau, Stepher Trees
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US-10-770-726-69
; Sequence 69, Application US/10770726
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Matches 174: Conserv
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                                                                                                            33 GQPFDVGPRY-TQLQYIGEGAYGMVSSAYDHVRKTRVAIKKI-SPFEHQTYCQRTLREIQ 90
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  Length 379,
Query Match 45.4%; Score 887; DB 7; Length 37 Best Local Similarity 50.0%; Pred. No. 4.6e-70; Matches 173; Conservative 65; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 45.0%; Score 878; DB 6; Length 36 Best Local Similarity 50.1%; Pred. No. 2.6e-69; Matches 174; Conservative 61; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 134, Application US/10878556A
Publication No. US20050266399A1
GENERAL INFORMATION:
APPLICANT: HOFFmann La-Roche Inc.
TITLE REFERENCE: 21762
CURRENT FILIGN NUMBER: US/10/878,556A
CURRENT FILING DATE: 2004-06-28
NUMBER OF SEQ ID NOS: 199
SOFTWARE: Patentin version 3.1
SEQ ID NO 134
LENGTH: 360
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PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: sw_hum/mk01_human
DATABASE ENTRY DATE: 1992-12-01
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US-10-878-556A-134
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145

73

Gaps

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Sequence 53, Application US/1077026

Publication No. US20050266409A1

GENERAL IPPORATION:
APPLICANT: Wyeth
APPLICANT: Liu, Weth
APPLICANT: Liu, Weth
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATIN
TITLE OF INVENTION: CANCERS
FILE REPRENCE: AM101079 (031896-010000)
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT PILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: Patentin version 3.2
SEQ ID NO 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 CHSRNVLHRDLKPQNLLINRNGELKLADFGLARAFGIPVRCYSAE------VVTLWYRP 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153 IHSANVIHRDLKPSNLLLMANCDLKICDFGLARP-----SSESDMMTEYVVTRWYRA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    205 PELLLINSTDYSAA-DVWSVGCIFMELINR-QPLFPGRDHMHQMRLITEVIGTPTDDEL-G 261
                                                                                                                                                                                                     142 PLYQILRGLKYIHSANVIHRDLKPSNLLLNANCDLKICDFGLARPSSESDMMTEYVVTRW 201
                                                                                                                                                                                                                                                                                                                                                                                                                                         YRAPELLLNSTDYSAADVWSVGCIFWELINRQPLFPGRDHMHQMRLITEVIGTPTDDELG 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FIR--NEDARKYMRHLPQYPRRTFASMFP-RVQPA-----ALDLIBRMLTFNPL 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    308 ORITVEEALDHPYLERLHDIADEPICLEPFSPDFEQKALNE-----DQMKQLIFNEAI 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               346 KRISVDDALQHPYINVWYDPA-EVEAPPPQIYD---KQLDEREHTIEEWKELIYKEVM 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 KYQPPIMPIGRGAYGIVCSVMNFETREMVAIKKIANAFNNDMDAKRTLREIKLLRHLDHE
                                                                                                                                                                                                                                                                                                                                                                            169 LLYQMLCGIKHLHSAGIIHRDLKPSNIVVKSDCTLKILDFGLARTAGTSFMTPYVVTRY
                                                                                                                                                                        23 DIFGNKFEVTNKYOPPIMPIGRGAYGIVCSVMNPETREMVAIKKIANAFNNDMDAKRTLR
                                                                                                                                                                                                                                                            83 EIKLLRHLDHENIIGIRDVI-PPPIPQAFNDVYIATELMDTDLHHIIRSNQELSERHCQY
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                                                                                        Length 422;
                                                                                 Query Match
33.4%; Score 653; DB 6; Length 422
Best Local Similarity 40.5%; Pred. No. 1.2e-49;
Matches 145; Conservative 68; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
CRGANISM: Homo sapiens
US-10-770-726-53
                  ORGANISM: Homo sapiens
US-10-857-780-21
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    TYPE: PRT
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APPLICANT: RATH, STETAND B.
APPLICANT: RAMBERS, STEFAN M.
APPLICANT: RAMBERS, STETAN M.
APPLICANT: RAMBERS, STETAN M.
APPLICANT: RENELAND, RIKARD HENRY
APPLICANT: RENELAND, RIKARD HENRY
APPLICANT: HOYAL-WRIGHTSON, CAROLYN R.
ITILE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS
ITILE OF INVENTION: THEREOF
ITILE OF INVENTION: THEREOF
CURRENT APPLICATION NUMBER: US/10/857,780
CURRENT PILING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: 60/490,234
PRIOR FILING DATE: 2003-11-25
PRIOR FILING DATE: 2003-11-25
NUMBER OF SEQ ID NOS: 4962
SOFTWARE PARENTIN VERSION 3.2
SEQ ID NOS: 4962
Publication No. US20050266409A1
GENERAL INFORMATION:
APPLICANT: Wyeth:
APPLICANT: Wyeth:
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AM10.079 (031896-010000)
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT APPLICATION NUMBER: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
SEQ ID NO 69
LENGTH: 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      188 YRAPEVILSWMHYNQTVDIWSVGCIMAEMLIGKTLFKGKDYLDQLLQILKVTGVPGTEFV 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 BIKLLRHLDHENIIGIRDVIPPPIP-QAFNDVYIATELMDTDLHHIIRSNQELSEEHCQY 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261 GPIRNEDARKYMRHLPQYPRRTPASMFPRVQPAALDLIERMLTFNPLQRITVEEALDHPY 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 DIFGNKFEVTNKYQPPIMPIGRGAYGIVCSVMNFETREMVAIKKIANAFNNDMDAKRTLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142 FLYQILRGLKYIHSANVIHRDLKPSNLLLNANCDLKICDFGLARPSSESDMMTEYVVTRW
                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
                                                                                                                                                                                                                                                                                                                                                                                                  DB 6; Length 365;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LERLHDIADEPICLEPFSFDFEQKALNEDQMKQLIFNEAIEMNPNIR 367
                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                Query Match 38.3%; Score 747.5; DB 6; Best Local Similarity 43.2%; Pred. No. 5.9e-58; Matches 150; Conservative 65; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-857-780-21
; Sequence 21, Application US/10857780
; Publication No. US20050272043A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-10-770-726-69
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Sequence 55, Application US/1077026
Publication No. US20050266409A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Weeth
APPLICANT: Liu, Wet
APPLICANT: Liu, Wet
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATINC
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AM101079 (031896-010000)
CURRENT APPLICATION UNMERE: US/10/770,726
CURRENT PILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: Patentin version 3.2
SEQ ID NO 55:
LENGTH: 346
                                                                                                                     9
                                                                                                                                                            42 IGRGAYGIVCSVMNFETREMVAIKKIANAFNNDMDAKRTLREIKLLRHLDHENIIGIRDV 101
                                                                                                                                                                                                                                       102 IPPPIPQAFNDVYIATELMDTDLHH-------IIRSNQELSEEHCQYFLYQILR 148
                                                                                                                                                                                                                                                                              70 I-----HTEWKLYLVFBFLHQDLKKFMDASALTGIPLPLIKS------YLFQLLQ 1113
                                                                                                                                                                                                                                                                                                                     149 GLKYIHSANVIHRDLKPSNLLLNANCDLKICDFGLARP-SSESDMMTEYVVTRWYRAPEL 207
                                                                                                                                                                                                                                                                                                                                              LINSTDYS-AADVWSVGCIFMELINRQPLFPGRDHMHQMRLJTBVIGTPTDDFLGFIRNE 266
                                                                                                                                                                                                                                                                                                                                                                                                                      97 GIRDVIPPPIPQAF---NDVYIATELMDTDLHHIIRSNQ-ELSEEHCQYFLYQILRGLKY 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 153 IHSANVIHRDLKPSNLLLNANCDLKICDFGLARP-SSESDMMTEYVVTRWYRAPBLLLNS 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RMYGVGVDMMANGCILAELLLRVPFLPGDSDLDQLTRIFETLGTPTEEGW------P 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 IGRGAYGIVCSVMNFETREMVAIKKIANAFNNDMDAK----RT-LREIKLLRHLDHENII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMPDYKPSFPKWARQDFSKVVPPLDEDGRSLLSQMLHYDPNKRISAKAALAHPFFQ 287
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                                                                              Length 298;
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                                                                              DB 6;
                                                                                                                     49; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 23.6%; Score 461; DB 6; Best Local Similarity 39.3%; Pred. No. 4.4e-33;
                                                                           23.9%; Score 467.5; DB 6 36.5%; Pred. No. 9.9e-34;
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                                                                                                                     Matches 108; Conservative
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-770-726-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                              Query Match
Best Local Similarity
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Publication No. US20050266409A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Brown, Eugene
APPLICANT: Brown, Eugene
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TILLE OF INVENTION: CANCERS
FILE REFERENCE: AM101079 (031896-010000)
CURRENT PILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: Patentin version 3.2
SEQ ID NO 51
LENGTH: 298
                                                                                                                                                                                                                                                                              FOR DIAGNOSING, PREVENTING, AND TREATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246 DLKQYLDDCGNIINMHNVKLFLFQLLRGLAYCHRQKVLHRDLKPQNLLINERGELKLADF 30S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IKKIANAFNNDMDAKRT-LREIKLLRHLDHENIIGIRDVIPPPIPQAFNDVYIATELMDT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 GLARPSS-ESDMMTEYVVTRWYRAPELLLINSTDYSA-ADVWSVGCIFMELINRQPLFPGR 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 DHMHQMRLITEVIGTPTDDEL-GFIRNEDARKYMRHLPQYPRRTFASMFPRVQPAALDLI 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             262 FIRNEDARKYMRHLPQYPRRT-FASMFPRVQPAALDLIERMLTFNPLQRITVEEALDHPY 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLHHIIRSNQELSEEH-CQYFLYQILRGLKYIHSANVIHRDLKPSNLLLNANCDLKICDF 181
                                           230 MTKLPDYKPY----PMYPATTSLVNVVPKLNATGRDLLQNLLKCNPVQRISAEEALQHPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 APVARFRPTMTHGGRYLLYDIFGNKFEVTNKYQPPIMPIGRGAYGIVCSVMNFBTREMVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 496;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58; Mismatches 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   299 ERMLTFNPLORITVERALDHPYL---ERLHDIAD 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 TKLLQPEGRNRISAEDAMKHPFFLSLGERIHKLPD 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 25.2%; Score 491.5; DB 6
Best Local Similarity 35.5%; Pred. No. 1.6e-35;
Matches 119; Conservative 58; Mismatches 135
                                                                                                                                                 Sequence 72, Application US/10770726
Publication No. US20050266409A1
GENERAL INFORMATION:
APPLICANT: Weth
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wet
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AM101079 (031896-010000)
CURRENT APPLICATION WUMBER: US/10/770,726
CURRENT FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: Patentin version 3.2
SEQ ID NO 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
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US-10-770-726-51
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APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Brown, Eugene
APPLICANT: Liu, Weil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
TITLE OF INVENTION: CANCERS
FILE REPERBURES ANIOTOTO (031896-010000)
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT PILING DATE: 2004-02-04
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PRIOR FILING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: PCT/JP00/05061
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US 60/183,322
PRIOR APPLICATION NUMBER: US 60/183,322
PRIOR FILING DATE: 1999-0-29
PRIOR FILING DATE: 1999-0-29
PRIOR FILING DATE: 2000-01-11
PRIOR PILING DATE: 2000-01-11
PRIOR PILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: JP 2000-183767
PRIOR PILING DATE: 2000-05-05
PRIOR FILING DATE: 2000-05-05
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SOFTWARE: Patentin version 3.2
SEQ ID NO 65
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Best Local Similarity 36.11
Matches 105; Conservative
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Best Local Similarity 31.3
Matches 103; Conservative
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APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AM101079 (031896-010000)
CURRENT APPLICATION WUMBER: US/10/770,726
CURRENT FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: Patentin version 3.2
SEQ ID NO 48
LENGTH: 297
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TITLE OF INVENTION: PHOSPHATASE
FILE REPERENCE: 06501-099002
CURRENT APPLICATION NUMBER: US/11/109,156
CURRENT FILING DATE: 2005-04-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23.4%; Score 457; DB 6; Length 297; 36.1%; Pred. No. 8e-33;
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PRIOR APPLICATION NUMBER: US/10/060,065
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Publication No. US20050250144A1
GENERAL INFORMATION:
                                                                                                              Sequence 48, Application US/10770726
Publication No. US20050266409A1
GENERAL INFORMATION:
APPLICANT: Wyeth
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Kelichi Nagai
Tetsuji Otsuki
Shin-Ichi Funahashi
Chiaki Senoo
Jun-Ichi Nezu
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APPLICANT: Takao Inogai
APPLICANT: Tetsuo Nishikawa
APPLICANT: Koji Hayashi
APPLICANT: Koji Hayashi
APPLICANT: Mon-Lot Yamamoto
APPLICANT: Shizuko Ishii
APPLICANT: Tomoyasu Sugiyama
APPLICANT: Tomoyasu Sugiyama
APPLICANT: Tetsuii Otsuki
APPLICANT: Kelichi Nagai
APPLICANT: Tetsuii Otsuki
APPLICANT: Shin-Ichi Funahashi
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Jun-Ichi Yamamoto
Shizuko Ishii
Tomoyasu Sugiyama
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Best Local Similarity 36.1%
Matches 105; Conservative
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 32.4%
Matches 104; Conservative
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ORGANISM: Homo sapiens
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Publication No. US20050261482A1

GENERAL INFORMATION:

APPLICANT: BAYER AG

TITLE OF INVENTION: REGULATION OF HUMAN SERINE-THREONINE PROTEIN KINASE

FILE REFERENCE: LLOSG4 FOREIGN COUNTRIES

CURRENT APPLICATION WUMBER: US 60/259,215

PRIOR APPLICATION NUMBER: US 60/259,215

PRIOR APPLICATION NUMBER: US 60/306,468

PRIOR PILING DATE: 2001-01-03

PRIOR PLING DATE: 2001-01-03

PRIOR PLING DATE: 2001-07-20

PRIOR APPLICATION NUMBER: US 60/306,908

PRIOR PLING DATE: 2001-07-30

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin version 3.1

LENGTH: 483
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                                                                                                                                                                                                                                                                                  FIRNEDARKYMRHLPQYPRRTFASMF-PRVQPAALDLIERMLTFNPLQRITVEEALDHPY 320
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                ------DVIPPPIPQAFNDVYIATELMDTDLHHIIRSNQELSEEHCQYF 142
                                                                                  116 FYSSGEKKDEVYLNLVLDYVPETVYRV------ARHYSRAKQTLPVIYVKLY 161
                                                                                                                                              261 GPIRNEDARKYMRHL-PQYPRRTFASM--------FPRVQPAALDL 297
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                                                                                                                             143 LYQILRGLKYIHSANVIHRDLKPSNLLLINAN-CDLKICDFGLARPSSESDMMTEYVVTRW
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IGRGAYGIVCSVMNPETREMVAIKKIANAFNNDMDAKRTLREIKLLRHLDHENIIGIR--
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31.0%; Pred. No. 6.8e-31;
tive 65; Mismatches 120;
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US-10-451-375-12
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Best Local Similarity
Matches 111; Conserva
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Sequence 49, Application US/1077026
Publication No. US20050266409A1
GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION: CANCERS
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT APPLICATION NUMBER: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: Patentin version 3.2
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Publication No. US20050266409A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Liu, Wei
TITLE OF INVENTION: CANCERS
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AM101079 (031896-010000)
CURRENT APPLICATION WUMBER: US/10/770,726
CURRENT FILING DATE: 2004-02-04
WUMBER OF SEQ ID NOS: 48640
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122 RQFLRGLDFLHANCIVHRDLKPENILVTSGGTVKLADFGLARIYSYQMALTPVVVTLMYR 181
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239 -PRDVSLPRGAFPPRGPRPVQSVVPEMEESGAQLILEMITFNPHKRISAFRALQHSYLHK 297
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Best Local Similarity 35.7%; Pred. No. 7.4e-31;
Matches 107; Conservative 49; Mismatches 131; Indels 13; Gaps
; ORGANISM: Homo sapiens
US-10-770-726-52
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Sequence 1342, Ap
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Sequence 13124, Ap
Sequence 1324, Ap
Sequence 1447, Ap
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Sequence 1313, Ap
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Sequence 137817,
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Sequence 1386, Ap
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34, Appl
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3: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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Sequence 42499, A
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Sequence 2, Application US/10768886
Publication No. US20040209325A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: Mitogen-Activated Protein Kinase and Method of Use to Enhance;
TITLE OF INVENTION: Mitogen-Activated Protein Kinase and Method of Use to Enhance;
TITLE OF INVENTION: Mitogen-Activated Protein Kinase and Method of Use to Enhance;
TITLE REPERBENCE: UAP-03-14
CURRENT APPLICATION NUMBER: US/10/768,886
CURRENT PILING DATE: 2004-01-31
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.2
SEQ ID NO 2.
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ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-768-886-2
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| Publication No. US20040214272A1
| Publication No. US20040214272A1
| GENERAL INFORMATION:
| APPLICANT: La Rosa Thomas J.
| APPLICANT: La Rovalic, David K.
| APPLICANT: Abou, Yihua
| APPLICANT: Zhou, Yihua
| TITLE OF INVENTION: Nacleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| CURRENT APPLICATION NUMBER: US/10/425,115
| CURRENT APPLICATION NUMBER: US/10/425,115
| CURRENT FILING DATE: 2003-04-28
| NUMBER OF SEQ ID NOS: 369326
| SEQ ID NO 191397
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US-10-732-923-1342

US-10-732-923-1342

Sequence 1342, Application US/10732923

Publication No. US20050108791A1

GENERAL INFORMATION:

APPLICANT: Edgerton, Michael D

TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES

FILE REPERENCE: 38-15(52796)C

CURRENT APPLICATION NUMBER: US/10/732,923

CURRENT APPLICATION NUMBER: 10/310,154

PRIOR FILING DATE: 2002-12-04

NUMBER OF SEQ ID NOS: 24149

SEQ ID NO 1342

LENGTH: 369

TYPE: PRI

TYPE: 
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93.2%; Score 1819.5; DB 5;
Best Local Similarity 91.3%; Pred. No. 7.5e-142;
Matches 337; Conservative 20; Mismatches 11;
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361 LELNPNPRY 369
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US-10-732-923-1342
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US-10-425-115-191397
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Sequence 45777, Application US/10767701
Sequence 45777, Application US/10767701
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
ITTLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
ITTLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
TITLE OF INVENTION: 1912535)B
CURRENT APPLICATION NUMBER: 1051407777101
CURRENT PILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 45777
LENGTH: 374
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                                                                                                                                                                                              DB 4; Length 397;
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US-10-767-701-45777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; FEATURE:
; OTHER INFORMATION; Clone ID: MRT4577_106134C.1.pep
US-10-425-115-191397
                                                                                                                                                                                           Query Match 90.9%; Score 1775.5; DB 4. Best Local Similarity 84.4%; Pred. No. 3.5e-138; Matches 335; Conservative 20; Mismatches 13;
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FEATURE:
NAME/KEX: unsure
CACTION: (1)..(397)
OTHER INFORMATION: unsure at all Xaa locations
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ORGANISM: Sorghum bicolor
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US-10-767-701-45777
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190 LARPNLENENMTEYVVTRWYRAPELLINSDYTEAIDVWSVGCIFWELMNRKPLFAGKDH 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MHOMRLITEVIGTPTDDELGFIRNEDARKYMRHLPQYPRRTFASMFPRVQPAALDLIERM 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 GGQFPEFPNIVTHGGQYVQYDIFGNFFEITTKYRPPIMPIGRGAYGIVCSVFNAELNEMV
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; Bequence 1446, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TANAGEMIC PLANTS WITH IMPROVED PHENOTYPES
; CURRENT PELLION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; RIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 1446
                                                                                                                                                                                                                                                                                                                                                                           DB 5; Length 375;
                                                                                                               APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REPERENCE: 38-15(52796) C
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 10/310,154
PRIOR PILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 24149
SEQ ID NO 1324
LENGTH: 375
                                                                                                                                                                                                                                                                                                                                                                                                            46; Indels
                                                                                                                                                                                                                                                                                                                                                                         Query Match 72.7%; Score 1461.5; DB 5
Best Local Similarity 72.7%; Pred. No. 2.8e-112;
Matches 264; Conservative 52; Mismatches 46;
                                                                  Sequence 1324, Application US/10732923; Publication No. US20050108791A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
; ORGANISM: Solanum tuberosum
US-10-732-923-1446
                                                                                                                                                                                                                                                                                                                       Capsicum annuum
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LNP 372
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                                                     JS-10-732-923-1324
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MVAIKKIANAFDNHMDAKRTLREIKLLRHLDHENIIGIRDVIPPPIPQAFNDVYIGTELM 125
                                   DTDLHHIIRSNQELSEEHCQYFLYQILRGLKYIHSANVIHRDLKPSNLLLLNANCDLKICD 180
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                                                                                                       181 FGLARPSSESDMMTEYVVTRWYRAPELLLNSTDYSAA-DVWSVGCIFMELINRQPLFPGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1332, Application US/10732923
Publication No. US20050108791A1
Publication No. US20050108791A1
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION:
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
TILE REPERBING: 38-15(52796)C
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 10/310,154
PRIOR PILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 24149
SEQ ID NO 1332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Nicotiana benthamiana
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                                                                      300 RMLTENPLORITVEBALDHPYLERLHDIADEPICLEPFSFDFEQKALNEDQMKQLIFNEA 359
61 MVAIKKIANAFNNDMDAKRTLREIKLLRHLDHENIIGIRDVIPPPIPQAFNDVYIATELM
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Publication No. US20050108791A1
GENERAL INFORMATION:
APPLICATY: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15 (52796)C
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT PILION DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 10/310,154
PRIOR FILING DATE: 2002-12-04
NUMBER: OF SEQ ID NOS: 24149
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Publication No. US20050108791A1
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSCENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REPERENCE: 38-15.52796.C
CURRENT APPLICATION NUMBER: US/10/732,923
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LAFNPEYQH 393
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LAFNPEYQH 392
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US-10-732-923-1334
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Publication No. US20050108791A1

GENERAL INFORMATION:

APPLICANT: Edgerton, Michael D

TITLE OF INVENTION: TRANSCENIC PLANTS WITH IMPROVED PHENOTYPES

FILE REFERENCE: 38-15(52796)C

CURRENT FILING DATE: 2003-12-10

PRIOR PLING DATE: 2003-12-04

NUMBER OF SEQ ID NOS: 24149

SEQ ID NO 1447
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     DB 5;
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   Query Match 74.2%; Score 1448.5; DB 5. Best Local Similarity 73.7%; Pred. No. 3.5e-111; Matches 269; Conservative 48; Mismatches 41;
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US-10-732-923-1447
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386 AFNPEYQH 393
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Best Local Similarity
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US-10-424-599-284784
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                                                                                                                                                                                                                                                                                                                                                  LITEVIGTPIDDELGFIRNEDARKYMRHLPQYPRRTFASMFPRVQPAALDLIERMLIFNP 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246 LITELIGTPTDSDLGSIQNENARRYIRQLPLRPRQQLANGFPHVHPLAIDLMDKMLTFNP 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 VAIKKIANAFNNDMDAKRTLREIKLLRHLDHENIIGIRDVIPPPIPQAFNDVYIATELMD 121
                                                                                                                                                                                                                                                                       68 ANAFNNDMDAKRILREIKLLRHLDHENIIGIRDVIPPPIPQAFNDVYIATELMDTDLHHI 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 PVAGIDNIPATISHGGRFIQYNIFGNVFEVTAKYKPPIMPIGKGAYGIVCSALNSETNEH 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188 SESDMMTEYVVTRWYRAPELLINSTDYSAA-DVWSVGCIFMELINROPLFPGRDHMHOMR
                                                                                                                                                                                                              8 BPRPTMTHGGRYLLYDIFGNKFEVTNKYQPPIMPIGRGAYGIVCSVMNFETREMVAIKKI
                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Publication No. US2005010879131

Publication No. US2005010879131

Publication No. US2005010879131

GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
TILE REFERENCE: 38-15(52796)C
CURRENT APPLICATION WUMBER: US/10/732,923

CURRENT FILING DATE: 2003-12-10
PRIOR FILING DATE: 2002-12-04

NUMBER OF SEQ ID NOS: 24149
                                                                                                                                                    Length 365;
                                                                                                                                                                               Indels
                                                                                                                                                                                 43;
                                                                                                                                                 73.2%; Score 1430; DB 5; 74.3%; Pred. No. 1.1e-109; iive 47; Mismatches 43;
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 10/310,154
PRIOR FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 24149
SEQ ID NO 1334
                                                                                                                                                                 Best Local Similarity 74.3% Matches 266; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) ORGANISM: Capsicum annuum
US-10-732-923-1323
                                                                                                       ; ORGANISM: Ipomoea batatas
US-10-732-923-1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-732-923-1323
                                                                           LENGTH: 365
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Anou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PLING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 SVMNFETREMVAIKKIANAFNNDMDAKRTLREIKLLRHLDHENIIGIRDVIPPPIPQAFN 111
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                                                                                                                             326 MLTFDPRRRLTVEDALAHPYLTSLHDISDEPVCTTPFSFDFEQHALTEEQMKELIYREGL 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DVYIATELMDTDLHHIIRSNQELSEEHCQYFLYQILRGLKYIHSANVIHRDLKPSNLLLN 171
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                                                                                                                                                                                                                      301 MLTFNPLQRITVEEALDHPYLERLHDIADEPICLEPFSFDFEQKALNEDQMKQLIFNEAI 360
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207 GLARVISETDEWIEYVVTRWYRPPELLLNSSDYTAAIDVWSVGCIFWELMDRRPLPPGRD
                                                                                            HWHOMRLITEVIGTPIDDELGFIRNEDARKYMRHLPQYPRRIFASMFPRVQPAALDLIER
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al Similarity 77.1%; Pred. No. 2.3e-102;
242; Conservative 46; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: PAT_MRT3847_99188C.1.pep
US-10-424-599-284784
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; Publication No. US20040031072A1
; GENERAL INFORMATION:
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US-10-767-701-45781
US-10-767-701-45781
US-10-767-701-45781
Sequence 45781, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: NUCleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT PILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 45781
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                                                                                                                                                                                                                                                       121 DTDLHHIIRSNQELSEEHCQYFLYQILRGLKYIHSANVIHRDLKPSNLLLNANCDLKICD 180
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                                                                                                                                                                                                                                                                                                                                                                                                        18 FGLARPSSESDMMTEYVVTRWYRAPELLLNSTDYSAAIDVWSVGCIFMELINRQPLFPGR 137
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                             MDGAPVAEFRPTMTHGGRYLLYD1FGNKFEVTNKYQPP1MP1GRGAYG1VCSVMNFETRE
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US-10-767-701-45781
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ORGANISM: Sorghum bicolor
                                                                                                                                                                                                    62 MVAIKKI-----
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Publication No. US20040209325A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
Mitogen-Activated Protein Kinase and Method of Use to Enhance
TITLE OF INVENTION:
GIOTOR:
GURRENT FILIS OF MAPER:
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           GENERAL INFORMATION:

APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Solou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: PLANTEN PLANTE and Uses Thereof for Plant Improvement
FILLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)8
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 49119
LENGTH: 318
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Best Local Similarity 71.5%; Pred. No. 5.7e-102;
Matches 264; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 68.6%; Score 1340.5; DB 4. Best Local Similarity 77.1%; Pred. No. 2.3e-102; Matches 242; Conservative 46; Mismatches 25;
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No. US2004003488BA1
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US-10-768-886-4
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SUMMARIES	ID	US-08-837-593-6	US-08-837-593-5	US-09-623-034-2	US-08-837-593-7	38-837-	US-08-837-593-3	US-08-837-593-2	US-08-837-593-8	US-09-828-313-34	US-08-837-593-9	US-09-739-455-13	US-09-739-455-23	US-10-153-919-13	US-10-153-919-23	US-09-417-197-57	US-08-176-620A-2	US-08-463-862-2	US-08-461-985-2	US-08-458-887-2	US-08-932-787B-2	US-08-932-012C-2	US-08-888-818C-2	US-08-176-620A-11	US-08-461-985-11	US-08-176-620A-14	US-08-461-985-14	US-09-487-558B-116
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US-08-459-953A-8 US-09-393-212-8 US-09-411-628-14 US-09-538-092-1021 US-09-538-092-1021 US-09-642-749-25 US-09-417-197-39 US-08-459-953A-9 US-08-459-953A-9 US-08-459-919-919 US-08-459-919-919 US-09-538-092-1028 US-09-538-092-1028 US-09-538-092-1028 US-09-538-092-1028 US-08-461-985-12	US-09-457-040B-4 US-08-622-277A-14
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BESULT INCOMENTATION:

APPLICANT: Stang Zhuqun
TITLE OF INVENTION:
APPLICANT: Alang Zhuqun
TITLE OF INVENTION:
APPLICANT: Alang Zhuqun
TITLE OF INVENTION:
APPLICANT: Alang Zhuqun
TITLE OF INVENTION:
ADDRESSE: Dam, Dorders:
ADDRESSE: Dam, Decree; Suite 720
COTTER: Philadelphia
STATE: Philadelphia
COMPUTER: Inch Market Street, Suite 720
STATE: Philadelphia
COMPUTER: Inch Street
COMPUTER:
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190 LARPNIENENTEYVVTRWYRAPELLLNSSDYTAAIDVWSVGCIFWELMNRKPLFGGKDH 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MHQMRLITEVIGTPTDDELGFIRNEDARKYMRHLPQYPRRTFASMFPRVQPAALDLIERM 301
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Batent No. 6/65128

Retent No. 6/65128

Retent No. 6/65128

REBERATION:
APPLICANT: Zhang, Shuqun
TITLE OF INVENTION: WETHOOS OF USING A PATHOGEN-ACTIVATABLE
TITLE OF INVENTION: WETHOOS OF USING A PATHOGEN-ACTIVATABLE
TITLE REPERENCE: RUT98-0073

CURRENT APPLICATION WHORER: US/09/623,034

CURRENT FILING DATE: 2000-08-24

PRIOR APPLICATION NUMBER: CT/US99/03882

PRIOR APPLICATION NUMBER: 6C1/US99/03882

PRIOR APPLICATION WHORER: 60/075,685

PRIOR FILING DATE: 1999-02-24
                                                                                                                                                                                                                                                                                                 10 GGQPPDFPSVLTHGGQYVQPDIFGNFFEITTKYRPPIMPIGRGAYGIVCSVLNTELNEWV
                                                                                                                                                                                                                                                                                                                                                               63 AIKKIANAFNNDMDAKRTLREIKLLRHLDHENIIGIRDVIPPPIPQAFNDVYIATELMDT
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                                                                                                                                                                                                                                                                       3 GAPVAEFRPTMTHGGRYLLYDIFGNKFEVTNKYQPPIMPIGRGAYGIVCSVMNFETREMV
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                                                                                                                                                                             75.4%; Score 1472.5; DB 1
72.5%; Pred. No. 3.2e-145;
tive 58; Mismatches 41;
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SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                               Query Match
Best Local Similarity 72.5¶
Matches 263; Conservative
                                                                                          internal
                       MOLECULE TYPE: protein HYPOTHETICAL: NO
TOPOLOGY: linear
                                                                FRAGMENT TYPE: 11
ORIGINAL SOURCE:
8-837-502
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370 LNP 372
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                                           HYPOTHETICAL:
ANTI-SENSE: N
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US-09-623-034-2
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APPLICANT: Klessig, Daniel F.
APPLICANT: Klessig, Daniel F.
APPLICANT: Shang Zhuqun
TITLE OF INVENTION: "NO. 5977442el Salicylic Acid Induced
TITLE OF INVENTION: "NO. 5977442el Salicylic Acid Induced
TITLE OF INVENTION: May Kinase and its Use for Enhanced Disease Resistance in Plant ONRESPONDER ADDRESSE:
ADDRESSE: P.C.
STREET: Acol Market Street, Suite 720
CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                    KIANAFNNDMDAKRTLREIKLLRHLDHENIIGIRDVIPPPIPQAFNDVYIATELMDTDLH 125
                                                                                                                                                                                                                           126 HIIRSNQELSBEHCQYFLYQILRGLKYIHSANVIHRDLKPSNLLLLNANCDLKICDFGLAR 185
                                                                                                                                                                                                                                                                                                                   129 QIIRSNQNLSDEHCQYFLYQILRGLRYIHSANIIHRDLKPSNLLLNANCDLKIIDFGLAR 188
                                                                                                                                                                                                                                                                                                                                                                                      244
                                                                                                                                                                                                                                                                                                                                                                                                           189 PTMESDPMTEYVVTRWYRAPELLINSSDYTSAIDVWSVGCIFMELMNKKPLFPGKDHVHQ 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               305 NPLORITVERALDHPYLERIHDIADEPICLEPFSFDFEGKALNEDOMKOLIFNEAIEMNP 364
                                                                                                               65
                                                                                                                                          9 VAEPPAVQTHGGQFVQYNVFGNLFEVTAKYRPPIMPIGRGAYGIVCSLLNTETNELVAVK 68
                                                                                                            6 VAEFRPTMTHGGRYLLYDIFGNKFEVTNKYQPPIMPIGRGAYGIVCSVMNFETREMVAIK
                                                                                                                                                                                                                                                                                                                                                                                  PSSESDMMTEYVVTRWYRAPELLINSTDY-SAADVWSVGCIFMELINRQPLFPGRDHMHQ
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                                                                   Gaps
                                                                     1;
                           DB 1; Length 371;
                                                                   Indels
                                                                       35;
                  Query Match
77.0%; Score 1504.5; DB 1
Best Local Similarity 74.4%; Pred. No. 1.4e-148;
Matches 268; Conservative 56; Mismatches 35;
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MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: BM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRESENG Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/837,593
FILING DATE: April 21, 1997
CLASSIPICATION NUMBER: 60/029,805
FILING DATE: October 25, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
REFISCOMMUNICATION NUMBER: 36,252
REFISCOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-837-593-5
; Sequence 5, Application US/08837593
; Patent No. 5977442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (215) 563-4044
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: United
ZIP: 19103-2307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX:
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Bequence 4, Application US/08837593
Sequence 4, Application US/08837593
Sequence 4, Application US/08837593
Sequence 4. Application US/08837593
Sequence 4. Applicant in Sequence 4. Applicant in Sequence 4. Applicant: APPLICANT: Zhang Zhuqun
TITLE OF INVENTION: Map Kinase and its Use for Enhanced Disease Resistance in Pla
TITLE OF INVENTION: Map Kinase and its Use for Enhanced Disease Resistance in Pla
CORRESPONDENCE ADDRESS:
ADDRESSES: Dann, Dorfman, Herrell and Skillman,
ADDRESSES: P.C.
STREET: 1601 Market Street, Suite 720
                                                                                                                                                                                                                                                                                125 DLHQIIRSNQSLSEEHCQYFLYQLLRGLKYIHSANIIHRDLKPSNLLLNANCDLKICDFG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185 LARPTSENDFWTEYVVTRWYRAPELLLNSSDYTAAIDVWSVGCIFWELMNRKPLFPGKDH 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MHOMRLITEVIGTPTDDELGFIRNEDARKYMRHLPQYPRRTFASMFPRVQPAALDLIERM 301
                                                                                                                                                                                                                         64
                                                                                                                                                                                                         DLHHIIRSNOELSBEHCOYFLYQILRGLKYIHSANVIHRDLKPSNLLLNANCDLKICDFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LARPSSESDMMTEYVVTRWYRAPELLLNSTDYSAA-DVWSVGCIFWELINRQPLFPGRDH
                                                                                                                                                                             3 GAPVAEFRPTMTHGGRYLLYDIFGNKFEVTNKYQPPIMPIGRGAYGIVCSVMNFETREMV
                                                                                                                         Gaps
                                                                       DB 1; Length 370;
                                                                                                                           40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: MA
COUNTRY: Wated States of America
ZIP: 19103-2307
COMPUTER READBAIL FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTERO VERSION 1.5
SOFTWARE: FASTERO VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/837,593
FILING DATE: April 21, 1997
CLASSIFICATION NUMBER: 60/029,805
FILING DATE: October 25, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E
NAME: Reed, Janet E
REGISTRATION NUMBER: 36,252
RETERENCE/DOCKET NUMBER: 36,252
RETERENCE/DOCKET NUMBER: 36,252
RELEPONE: (215) 563-4100
TELEPRAKE: (215) 563-4100
                                                                  Query Match 75.3%; Score 1471.5; DB Best Local Similarity 72.7%; Pred. No. 4e-145; Matches 264; Conservative 58; Mismatches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LNP 367
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ORIGINAL SOURCE:
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US-08-837-593-7
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APPLICANT: Klessig, Daniel F.
APPLICANT: Abang Zhuqun
TITLE OF INVENTION: "No. 5977442el Salicylic Acid Induced
TITLE OF INVENTION: Map Kinase and its Use for Enhanced Disease Resistance in Plan
NUMBER OF SEQUENCES:
ADDRESSEE: Darn, Dorfman, Herrell and Skillman,
ADDRESSEE: P.C.
STREET: 1601 Market Street, Suite 720
CITY: Philadelphia
STREET: 1601 Market Street, Suite 720
CITY: Philadelphia
STREET: Diskette
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: DS
SOFTWARE: PastESQ Version 1.5
CUASSTRICATION NUMBER: US/08/837, 593
FILING DATE: April 21, 1997
CLASSTRICATION DATA:
APPLICATION NUMBER: 06/029,805
FILING DATE: October 25, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRALING JANET E.
REGISTRALING JANET E.
REGISTRALING DATE: PHILAGE DATE: PHILA
                                                                                                                                                                                                                                                                                                                                                                                                                    123 DLHHIIRSNQELSEEHCQYFLYQILRGLKYIHSANVIHRDLKPSNLLLNANCDLKICDFG 182
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                                                                                                                                                                                                                                                                                                                                             AIKKIANAFNNDMDAKRTLREIKLLRHLDHENIIGIRDVIPPPIPQAFNDVYIATELMDT 122
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                                                                                                                                                                                                                                       LARPNIENENWIEYVVTRWYRAPELLLNSSDYTAAIDVWSVGCIFWELMNRKPLFGGKDH
                        LARPSSESDMMTEYVVTRWYRAPELLLNSTDYSAA-DVWSVGCIFMELINRQPLFPGRDH
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Patent No. 5977442
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: RU
TELECOMMUNICATION INPORMATION:
TELEPHONE: (215) 563-4044
TELEPAX: (215) 563-4044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 370 amino acids
TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
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LNP 372
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US-08-837-593-2

US-08-837-593-2

Sequence 2, Application US/08837593

Patent No. 597442

GENERAL INFORMATION:

APPLICANT: Zhang Zhugun

TITLE OF INVENTION: "No. 5977442el Salicylic Acid Induced

TORRESPONDENCE ADDRESS: 14

CORRESPONDENCE ADDRESS: 14

ADDRESSEE: Dann, Dorfman, Herrell and Skillman,

ADDRESSEE: P.C.

TENER: LOI MARKET Street, Suite 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 VAIKKIANAFNNDMDAKRTLREIKLLRHLDHENIIGIRDVIPPPIPQAFNDVYIATELMD 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86 VAIKKIANAFDNKIDAKRTLREIKLLRHMDHENIVAIRDIIPPPQREAFNDVYIAYELMD 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TDL/HHIRSNQELSEEHCQYFLYQILRGLKYIHSANVIHRDLKPSNLLLNANCDLKICDF 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 GLARPSSESDMMTEYVVTRWYRAPELLLNSTDYSAA-DVWSVGCIFMELINRQPLFPGRD 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                206 GLARVISETDPMIEXVVIRMYRAPELLLINSSDYTAAIDVWSVGCIFMELMDRKPLFPGRD 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HMHQMRLITEVIGTPTDDELGFIRNEDARKYMRHLPQYPRRTFASMFPRVQPAALDLIER 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 PVAGIDNIPATLSHGGRFIQYNIFGNIFEVTAKYKPPIMPIGKGAYGIVCSALNSETNEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 PVA---EFRPTMTHGGRYLLYDIFGNKFEVTNKYQPPIMPIGRGAYGIVCSVMNFETREM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146 TDLHQIIRSNQGLSEEHCQYFLYQILRGLKYIHSANVLHRDLKPSNLLLNANCDLKICDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 74.0%; Score 1445.5; DB 1
Best Local Similarity 72.6%; Pred. No. 2.3e-142;
Matches 267; Conservative 52; Mismatches 44;
   PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/029,805
FILING DATE: OCCADER 25, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet B.
REGISTRATION NUMBER: 36,25
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-410
                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              || ::
385 AFNPEYQH 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO FRAGMENT TYPE: 1 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122
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| Sequence 3, Application US/08837593
| Patent No. 5977442
| GENERAL INFORMATION:
| APPLICANT: Zhang Zhuqun
| TITLE OF INVENTION: "No. 5977442el Salicylic Acid Induced
| TITLE OF INVENTION: "No. 5977442el Salicylic Acid Induced
| TITLE OF INVENTION: Map Kinase and its Use for Enhanced Disease Resistance in Plan
| NUMBER OF SEQUENCES: 14
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Dann, Dorfman, Herrell and Skillman,
| STATE: Philadelphia
| STATE: Philadelphia
| STATE: Philadelphia
| STATE: Dann, Dorfman, Do
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 PETREMVAIKKIANAFNNDMDAKRTLREIKLLRHLDHENIIGIRDVIPPPIPQAFNDVYI 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135 AYELMDTDLHQIIRSNQALSEEHCQYFLYQILRGLKYIHSANVLHRDLKPSNLLLNANCD 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LPPGRDHMHQMRLITEVIGTPTDDELGFIRNEDARKYMRHLPQYPRRTFASMFPRVQPAA 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 DGAP-----VAEFRPTMTHGGRYLLYDIFGNKFEVTNKYQPPIMPIGRGAYGIVCSVMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SETNEHVAVKKIANAFDNKIDAKRTLREIKLIRHMDHENVVAIRDIVPPPQREVFNDVYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 ATELMDTDLHHIIRSNQELSEEHCQYFLYQILRGLKYIHSANVIHRDLKPSNLLLNANCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LKICDFGLARPSSESDMMTEYVVTRWYRAPELLLNSTDYSAA-DVWSVGCIFMELINRQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45;
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

74.1%; Score 1448; DB 1;
Best Local Similarity 71.6%; Pred. No. 1.2e-142;
Matches 265; Conservative 52; Mismatches 45;
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 387 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DOLLOGY: HAPOTHETICAL: NO
                                                                                                                                                                                                                                                                                 internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IFNEAIEMNP 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   374 IYREALAFNP 383
                                                                                                                                                                                                                                                                              FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                     2
                                                                                                                                                                                                                                                     ANTI-SENSE:
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US-08-837-593-3
                                                                                                                                                                                                                                                                                                                                           US-08-837-593-4
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TITLE OF INVENTION: "NO. 5977442el Salicylic Acid Induced
TITLE OF INVENTION: Map Kinase and its Use for Enhanced Disease Resistance in Pla:
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 GNAFENRIDAKKTLREIKCLSHMDHENIIKIKDIVRPPDREEFNDVYIVYELMDTDLHQI 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SESDMMTEYVVTRWYRAPELLLINSTDYSAA-DVWSVGCIFMELINRQPLFPGRDHMHQMR 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190 SEADFWIEYVVTRWYRAPELLLINCTEYTAAIDIWSVGCILMELIKREPLFPGRDYAQQLG 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 ANAFNNDMDAKRTLRRIKLLRHLDHENIIGIRDVIPPPIPQAFNDVYIATELMDTDLHHI 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IRSNOELSEEHCQYFLYQILRGLKYIHSANVIHRDLKPSNLLLLNANCDLKICDFGLARPS 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                247 LITEVIGTPTDDELGFIRNEDARKYMRHLPQYPRRTFASMFPRVQPAALDLIERMLTFNP 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 BIKGIPTHEGKYVEYNVLGNPFEVTSKYIPPIQPVGRGAYGMVCCATNSETKEEVAIKKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 BFRPTMTHGGRYLLYDIFGNKFEVTNKYQPPIMPIGRGAYGIVCSVMNFETREMVAIKKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                   ADDRESSEE: Dann, Dorfman, Herrell and Skillman, ADDRESSEE: P.C.
STREET: 1601 Market Street, Suite 720
CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68.0%; Score 1327.5; DB 1
66.9%; Pred. No. 4.5e-130;
tive 59; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rutgers 97-0016
                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEM: DOS
SOFTWARET APPLICATION DATA:
APPLICATION NUMBER: US/08/837,593
FILING DATE: APATI 21, 1997
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/029,805
FILING DATE: OCCODER 25, 1996
ATTORNEY/AGENT INFORMATION:
NAMME: Reed, Janet B.
REGISTRATION NUMBER: 36,222
                                                                                                                                                                                                                                            United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: RUI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
                 APPLICANT: Klessig, Daniel F. APPLICANT: Zhang Zhugun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                371 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 66.9 Matches 240; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                           ZIP: 19103-2307
COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRAGMENT TYPE: : ORIGINAL SOURCE: US-08-837-593-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 MVAIKKIANAFNNDMDAKRTLREIKLLRHLDHENIIGIRDVIPPPIPQAFNDVYIATELM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         145 DIDLHQIIRSNQGLSEEHCQYFLYQILRGLKYIHSANVLHRDLKPSNLLLNANCDLKICD 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DHMHQMRLITEVIGTPTDDELGFIRNEDARKYMRHLPQYPRRTFASMFPRVQPAALDLIE 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            265 DHVHQLRLIMELIGTPSRAEMEPL-NENAKRYIRQLPLYRRQSFTEKFPHVHPTAIDLVE 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300 RMLTFNPLQRITVEEALDHPYLERLHDIADEPICLEPFSFDFEQKALNEDQMKQLIFNEA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MDGAPVAEFRPTWTHGGRYLLYDIFGNKFEVTNKYQPPIMPIGRGAYGIVCSVMNFETRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73.7%; Score 1438.5; DB 1; Length 393; 72.4%; Pred. No. 1.2e-141; tive 50; Mismatches 45; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                REPERENCE/DOCKET NUMBER: Rutgers 97-0016
FELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/837,593
FILING DATE: April 21, 1997
CLASSIFICATION:
                     United States of America
                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/029,805
FILING DATE: October 25, 1996
ATTORNEY, AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
US-08-837-593-8
; Sequence 8, Application US/08837593
; Patent No. 5977442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 393 amino acida
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (215) 563-4044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 72.44
Matches 267; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        360 IEMNPNIRY 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ropology: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
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65 KKIANAFNNDMDAKRTLREIKLLRHLDHENIIGIRDVIPPPIPQAFNDVYIATELMDTDL 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HHIIRSNQELSEEHCQYFLYQILRGLKYIHSANVIHRDLKPSNLLLNANCDLKICDFGLA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RPSSESD-MMTEYVVTRWYRAPELLLNSTDY-SAADVWSVGCIFMELINROPLFPGRDHM 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243 HOMRLITEVIGTPTDDELGFIRNEDARKYMRHLPQYPRRTFASMFPRVQPAALDLIERML 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 NQLKLIINILGSQREEDIBFIDNPKARKYIKSLPYSPGTPFSRLYPHAHPLAIDLLQRML 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  303 TENPLORITVERALDHPYLERLHDIADEPICLEPPSFDFEOKALNEDQMKQLIFNEAIEM 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 PVEPPNGIRTPGKHY--YSMWQSLFBIDTKY-VPIKPIGRGAYGIVCSSVNRETNEKVAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 PVABFRPTMTHGGRYLLYDIFGNKFEVTNKYQPPIMPIGRGAYGIVCSVMNFETREMVAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.8%; Score 1031; DB 1; 54.7%; Pred. No. 4.4e-99; tive 68; Mismatches 90;
                                                       MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOCTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/837,593
FILING DATE: April 21, 1997
CLASSIFICATION: 336
PRIOR APPLICATION UNMBER: 60/029,805
FILING DATE: October 25, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E
REFERENCE/DOCKET NUMBER: Rttgers 97-0016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13, Application US/09739455
Patent No. 6413756
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: RUTELECOMMUNICATION INFORMATION:
    ĕ
                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 372 amino acida
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 198; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein HYPOTHETICAL: NO
                 ZIP: 19103-2307
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO FRAGMENT TYPE: ORIGINAL SOURCE: US-08-837-593-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :|
HP 361
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APPLICANT: Xleady, Daniel F.
APPLICANT: Xleady Zhuqun
TITLE OF INVENTION: Mo. S977442el Salicylic Acid Induced
TITLE OF INVENTION: Map Kinase and its Use for Enhanced Disease Resistance in Plan
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman,
ADDRESSEE: P.C.
STRETT: 1601 Market Street, Suite 720
CITY: Philadelphia
STATE: PA
                                                                                               Sequence 34, Application US/09828313
Sequence 34, Application US/09828313
GENERAL INFORMATION:
APPLICANT: COSTA = SILVA, OSWALDO DA
APPLICANT: BCHNERT, HANS J.
APPLICANT: THIELEN, NOCHA VAN
APPLICANT: CHEN, ROUYING
TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED PROTEINS AND METHODS OF
TITLE OF INVENTION: USE IN PLANTS
TITLE OF INVENTION: USE IN PLANTS
TITLE OF INVENTION: UNBER: US/09/828,313
CURRENT APPLICATION NUMBER: 05/196,001
FRIOR PILING DATE: 2001-04-06
FRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 128
SOFTWARE: PATENTIN VET: 2.1
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  AKRITVEDALNHPFLISLHEINEEPVCDSPFNFDFEQASLSEDDIKELIWNEALKFDPN 368
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64.5%; Score 1260.5; DB 2
Best Local Similarity 64.7%; Pred. No. 4.6e-123;
Matches 233; Conservative 55; Mismatches 71;
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Patent No. 5977442
GENERAL INFORMATION:
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US-09-828-313-34
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LENGTH: 375
TYPE: PRT
                                                                               US-09-828-313-34
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Sequence 23, Application US/10153919
Fatent No. 6858420
GENERAL INFORMATION:
APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THERROF
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; Patent No. 6858420
; Patent No. 6858420
; GENERAL INFORMATION:
; APPLICATION:
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: THEREOF
; TITLE OF INVENTION: THEREOF
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO00653DIV
; CURRENT APPLICATION NUMBER: 05/24
; PRIOR PILLING DATE: 2002-05-24
; PRIOR PILLING DATE: 2000-06-06
; PRIOR PILLING DATE: 2000-06-06
; PRIOR PILLING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) ORGANISM: Dictyostelium discoideum US-10-153-919-13
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US-10-153-919-23
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US-10-153-919-13
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Batent No. 6413756
GENERAL INFORMATION:
APPLICANT: YAN, Chunhua et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND ITTLE OF INVENTION: THERROF
FILE REFERENCE: CLOOGES3
CURRENT APPLICATION NUMBER: US/09/739,455
CURRENT FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 23
APPLICANT: YAN, Chunhua et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
CURRENT APPLICATION WUMBER: US/09/739,455
CURRENT APPLICATION DATE: 2000-12-19
SOFTWARE: FASISEO FOR WINDOWS VERSION 4.0
SEO ID NO 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 47.2%; Score 921.5; DB 2; Best Local Similarity 59.2%; Pred. No. 9.1e-88; Matches 174; Conservative 52; Mismatches 63;
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                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Dictyostelium discoideum
US-09-739-455-13
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Matches 174; Conservative
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US-09-739-455-23
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Search completed: December 27, 2005, 20:42:00
Job time : 47 secs
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Sequence 5.8 Application US/09417197

Patent No. 6518021

GENERAL INFORMATION:

APPLICANT: Ole THAGTRUP, et al.

TITLE OF INVENTION: On A Cellular Response

TITLE OF INVENTION: On A Cellular Response

FILE REPRESENCE: 3759-0110P

CURRENT APPLICATION NUMBER: US/09/417,197

CURRENT FILING DATE: 1999-10-07

NUMBER OF SEQ ID NOS: 143

SOFTWARE: PatentIn version 3.0

SEQ ID NO 57

LENGTH: 624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42 IGRGAYGIVCSVMNFETREMVAIKKIANAFNNDMDAKRTLREIKLLRHLDHENIIGIRDV 101
                                                                                                                                                                                                                                                                                                                                                                                                      DLKPSNLLLLNANCDLKICDFGLAR--PSSESDMMTEYVVTRWYRAPELLLNSTDYS-AAD 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 GNKFEVTNKYQPPIMPIGRGAYGIVCSVMNFETREMVAIKKIANAFNNDMDAKRTLREIK 85
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                                                                                                                                                                                                                                        63;
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Best Local Similarity 59.2%; Pred. No. 9.1e-88;
Matches 174; Conservative 52; Mismatches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INPORMATION: MERK1-P64L-S65T-GFP fusion
PRIOR APPLICATION NUMBER: 60/209,585
PRIOR FILING DATE: 2000-06-06
PRIOR APPLICATION NUMBER: 09/739,455
PRIOR PILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PASTERO for Windows Version 4.0
SEQ ID NO 23
LENGTH: 304
                                                                                                                                     ; TYPE: PRT
; ORGANISM: Dictyostelium discoideum
US-10-153-919-23
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Best Local Similarity 50.9%
Matches 175; Conservative
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YRAPELLLNSTDYS-AADVWSVGCIFWELINRQPLFPGRDHMHQMRLITEVIGTFTDDEL 260
                  211 YRAPRIMINSKGYTKSIDIWSVGCILAEMLSNRPIFFGKHYLDQLNHILGILGSPSQEDL 270
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December 27, 2005, 20:30:11; Search time 39 Seconds (without alignments) 907.892 Million cell updates/sec
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1953
1 MDGAPVAEFRPTWTHGGRYL......DQMKQLIFNEAIEMNPNIRY 368
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                        283416 seqs, 96216763 residues
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Gapop 10.0 , Gapext 0.5
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Perfect score:
Sequence:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000 PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	mitogen-activated	protein kinase MMK	mitogen-activated	hypothetical prote	mitogen-activated	hypothetical prote	probable protein k	mitogen-activated	probable mitogen-a	mitogen-activated	mitogen-activated	mitogen-activated,	protein F14N23.9 [	MAP kinase (ATMPK7	mitogen-activated	protein T30E16.13	MAP kinase like pr	pathogenicity MAP	mitogen-activated										
SUMMARIES	QI	856638	T09622	T47504	T03971	S40469	S48123	S51321	S40472	T14915	833635	S51320	S60121	S40470	C86146	S40471	C86214	T13024	T47803	D84898	839559	A56042	S52989	F86236	B84561	S40473	F96619	C85430	T51944	T51943
	Query Match Length DB		371 2		375 2									376 2	369 2		363 2			406 2	•	•			368 2	368 2		361 2	356 2	361 2
df	Query	93.2	77.0	75.4	75.4	75.3	74.1	74.0	73.8	73.8	73.6	68.0	67.9	67.4	65.4	64.4	63.7	63.0	62.9	62.0	52.8	52.4	52.1	50.2	50.1	49.8	49.5	48.1	47.3	46.4
	Score	1819.5	1504.5	1472.5	1472.5	1471.5	1448	1445.5	1442	1441.5	1437	1327.5	1325.5	1315.5	1277.5	1257.5	1244.5	1230	1229	1210.5	1031	1024	1017	186	979	972	996	940	923.5	906
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Ca2+/calmodulin-de	Ca2+/calmodulin-de	extracellular sign	Ca2+/calmodulin-de	MAP kinase mpk-1 (	MAP kinase sur-1 (	protein kinase (EC	protein kinase (EC	MAP kinase 3 (EC 2	MAP kinase 1 (EC 2	mitogen-activated	protein kinase (EC	protein kinase ERK	extracellular sign	mitogen-activated	protein kinase ERK
S28184	JC1451	JW0052	A60041	A36978	A36977	S15663	S28548	A48082	JQ1400	S16444	A40033	S25011	JW0053	A39754	A47211
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377	380	392	369	376	444	372	353	379	360	358	358	360	369	361	362
46.3	46.2	46.2	46.1	46.0	46.0	45.9	45.8	45.4	45.0	44.9	44.9	44.9	44.9	44.1	43.8
40	902	905	901	868	868	897	894	887	878	877	877	877	877	862	855.5
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## ALIGNMENTS

# W E Z O O O	RESULT 1 S56638 mitogen-activated protein kinase 1 homolog (clone Agpk9) - oat N,Alternate names: MAP1 kinase C;Species: Avana sativa (oat) C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004 C;Accession: S56638
	R.Huttly, A.K.; Phillips, A.L. Plant Mol. Biol. 27, 1043-1052, 1995 A.Title: Gibberellin-regulated expression in oat aleurone cells of two kinases that sho A.Faference number: S56638; MUID:95284341; PMID:7766874 A.Accession: S56638
	A:Status: nucleic acid sequence not shown A:Molecule type: mRNA A:Residues: 1-369 <hut></hut>
	A;Cross-references: UNIPROT:Q43379; UNIPARC:UPI00000AA427; EMBL:X79993; NID:g871983; PI CS:Superfamily: Kinase-related transforming protein; protein Kinase homology C;Keywords: ATP; phosphotransferase; protein; protein Kinase homology <kin>. P:33-322/Domain: protein kinase homology <kin>.</kin></kin>
_	F;42-50/kegion: procein kinase Air-binging mocii Chiery March 93 2*: Score 1819.5: DB 2: Length 369:
	Similarity 91.3%; Pred. No. 7.3e-69; 7; Conservative 20; Mismatches 11; I
	Qy 1 MDGAPVAEFRPTWITHGGRYLLYDIFGNKFEVTNKYQPPIMPIGRGAYGIVCSVMNFETRE 60
	Db 1 MDGAPVAEFRPIMTHGGRFLLYNIFGNQFEITSKYQPPIMPIGRGAYGIVCSVMNFETRE 60
	Qy         61 MVAIKKIANAFNNDMDAKRTLREIKLIAHLDHENIIGIRDVIPPIPQAFNDVYIATELM 120           Dh         61 MVAIKKIANAFNNMDAKRTI.REIKII.RHI.DHENIVGI.RDVIPPSI POSINDVYIATELM 120
	121 DIDLHHIIRSNQELSEEHCQYFLYQILRGLKYIHSANVIHRDLKPSNLLLNANCDLKICD
	DD 121 DTDLHHIIRSNQELSEEHCQYFLYQLLRGLKYIHSANVIHRDLRPSNLLLNANCDLKICD 180
	Qy 181 PGLARPSESDMMTEYVVTRWYRAPELLLNSTDYSAA-DVWSVGCIFMELINRQPLFPGR 239
	Db 181 FGLARPSSESDMMTEYVVTRWYRAPELLLINSTDYSAAIDVWSVGCIFMELINRAPLFPGR 240
	Qy 240 DHWHQMRLITEVIGTPTDDELGFIRNEDARKYMRHLPQYPRRTFASMFPRVQPAALDLIE 299
	GFIRNEDARRYMRHI
	Qy 300 RMLTFNPLQRITVBEALDHPYLBRLHDIADBPICLEPFSFDFEQKALNEDQMKQLIFNEA 359
_	YLERLHDVADEPIC
	Qy 360 IEMNPHIRY 368
_	Db 361 LELNPNFRY 369

241

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Gaps

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A;Molecule type: mRNA
A;Residues: 1-375 <SEO.
A;Cross-references: UNIPROT:Q40598; UNIPARC:UPI00000A4FF8; EMBL:D61377; NID:g1136297; P]
C;Comment: MAP kinase is part of the initial response of higher plants to mechanical wou
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mitogen-activated protein kinase (BC 2.7.1.-) WIPK - common tobacco C; Species: Nicotiana tabacum (common tobacco)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T0391,
R;Geo, S.; Okamoto, M.; Seto, H.; Ishizuka, K.; Sano, H.; Ohashi, Y.
Science 270, 1988-1992, 1995
A;Title: Tobacco MAP kinase: a possible mediator in wound signal transduction pathways. A;Reference number: Z1570; MUID:96123271; PMID:8533090
                                                                                                                                                                                                                                    AIKKIANAFNNDMDAKRTLREIKLLRHLDHENIIGIRDVIPPPIPQAFNDVYIATELMDT 122
                                                                                                                                                                                                                                                                                                                                                DLHHIIRSNQELSEEHCQYFLYQILRGLKYIHSANVIHRDLKPSNLLLNANCDLKICDFG 182
                                                                                                                                                                                                                                                                                                                                                                             MHOMRLITEVIGTPTDDELGFIRNEDARKYMRHLPQYPRRTFASMFPRVQPAALDLIERM 301
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                                                                                                                                                          GGQYTDFPAVETHGGQFISYDIFGSLFBITSKYRPPIIPIGRGAYGIVCSVLDTETNELV
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                                                                                                                             GAPVAEFRPTWTHGGRYLLYDIFGNKFEVTNKYQPPIMPIGRGAYGIVCSVMNFETREMV
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                 Length 370;
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                   DB 2;
                                                                       40;
                 Score 1472.5; DB
Pred. No. 1.5e-54;
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75.4%; Scor.
72.7%; Pred. No. 1...
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Best Local Similarity 72.5$
Matches 263; Conservative
                 Query Match
Best Local Similarity 72.74
Matches 264; Conservative
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LNP 367
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                                                                                     C;Species Medicago sativa (BC 2.7.1.-), cold- and drought-induced - alfalfa
C;Species: Medicago sativa (alfalfa)
C;Species: Medicago sativa (alfalfa)
C;Species: Medicago sativa (alfalfa)
C;Species: Medicago sativa (alfalfa)
C;Species: Medicago sativa
C;Species: Medicago sativa
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C;Species: Medicago sativa
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NiAlternate names: protein F9K21.220
CiSpecies: Arabidopsis thaliana (mouse-ear cress)
CiSpecies: Arabidopsis thaliana (mouse-ear cress)
CiDate: O-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
CiAccession: T47504
RiJordan, N. i Bangert, S.; Wisdelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Lemcke, K. submitted to the Protein Sequence Database, Pebruary 2000
A;Reference number: 224467
A;Reference number: 224467
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-370 <-JOR>
A;Reperimental source: cultivar Columbia; BAC clone F9K21
A;Reperimental source: cultivar Columbia; BAC clone F9K21
A;Introns: 53/2; 96/3; 142/3; 253/3; 315/1
A;Note: F9K21.220
C;Superfamily: kinase-related transforming protein; protein kinase homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 QIIRSNQNLSDEHCQYFLYQILRGLRYIHSANIIHRDLKPSNLLLNANCDLKIIDFGLAR 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244
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Best Local Similarity 74.4%; Pred. No. 7e-56;
Matches 268; Conservative 56; Mismatches 3
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Dacession: S40469
R;Mizoguchi, T.; Hayashida, N.; Yamaguchi-Shinozaki, K.; Kamada, H.; Shinozaki, K.
FRBS Lett. 316, 440-444, 1993
A;Title: ATMFKS: a gene family of plant MAP kinases in Arabidopsis thaliana.
A;Reference number: S40469, MUID:94109583; PMID:8282107
A;Recession: S40469
A;Molecule type: mRNA
A;Residues: 1-370 cMIZ>
A;Cross-references: UNIPROT:Q39023; UNIPARC:UPI000014C688; EMBL:D21839; NID:9457397; PIC
C;Genetics:
A;Gene:
C;Genetics:
A;Gene:
C;Genetics:
A;Gene:
A;Gene:
C;Genetics:
A;Gene:
A;Gene:
C;Reywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;35-324/Domain: protein kinase homology cKIR>
F;44-52/Region: protein kinase ATP-binding motif
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LTFNPLQRITVERALDHPYLERLHDIADEPICLEPFSFDFEQKALNEDQMKQLIFNEAIB
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LNP 367
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A,Molecule type: mRNA
A,Rebidues 1-387 «JON»
A,Erebidues 1-387 «JON»
A,Cross-references: UNIPROT:Q07176; UNIPARC:UPI000012F26C; EMBL:X66469; NID:g298018; PI)
R,Duerr, B.; Gawienowski, M.; Ropp, T.; Jacobs, T.
R,Duerr, B.; Gawienowski, M.; Ropp, T.; Jacobs, T.
A)Title: MsERKI: a mitogen-activated protein kinase from a flowering plant.
A,Reference number: S59949; MUID:93177216; PMID:8439746
                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-387 < DUE>
A;Cross-references: UNIPARC:UPI000012F26C; EMBL:L07042; NID:g289124; PIDN:AAB41548.1; P
C;Genetics:
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mitogen-activated protein kinase 4 (EC 2.7.1.-) - common tobacco
NyAlternate names: serine/threonine-ppecific protein kinase p45Ntf4
C;Species: Nicotiana tabacum (common tobacco)
C;Date: O'May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: $68190; $51321
R;Wilson, C.; Anglmayer, R.; Vicente, O.; Heberle-Bors, E.
R;Wilson, C.; Anglmayer, R.; Vicente, O.; Heberle-Bors, A;Ritle: Molecular cloning, functional expression in Escherichia coli, and characteriza A;Reference number: $68189; MUID:96061956; PMID:7588752
                                                                                                                                    and
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004 C;Accession: S48123; S59949 R;Jonak, C.; Pay, A.; Boegre, L.; Hirt, H.; Heberle-Bors, R. Plant J. 3, 61-67, 1993 A;Til-le: The plant homologue of MAP kinase is expressed in a cell cycle-dependent A;Reference number: S48123; MUID:94035163; PMID:8220466 A;Accession: S48123.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: kinase-related transforming protein; protein kinase homology C;Keywords: ATP; phosphotransferase; protein kinase P;52-340/Domain: protein kinase homology <KIN>F;61-69/Region: protein kinase ATP-binding motif
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Pred. No. 1.6e-53;
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Best Local Similarity 71.6%;
Matches 265; Conservative 5:
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A; Molecule type: mRNA A; Residues: 1-393 <WIL> A;Accession: S68190

mitogen-activated protein kinase 7 (BC 2.7.1.-) - alfalfa N;Alternate names: MAP kinase; MsK7 kinase C;Species: Medicago sativa (alfalfa)

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A; Residues: 1-371 < LIG>
A; Residues: 1-371 < LIG>
A; Cross-references: UNIPROT:004694; UNIPARC:UPI00000A9255; EMBL:Y12785; NID:g2231033; PI
A; Cross-references: UNIPROT:004694; UNIPARC:UPI0000A9255; EMBL:Y12785; NID:g2231033; PI
C; Comment: MAP kinase is part of the initial response of higher plants to mechanical wou C; Superfamily: kinase-related transforming protein; protein kinase homology C; Keywords: ATP; phosphotransferase
F; 36-325/Domain: protein kinase homology < KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mitogen-activated protein kinase I (BC 2.7.1.-) - parsley
NyAlternate names: MAP kinase I
CiSpecies: Petroselinum crispum (parsley)
CiDate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
CiDate: 20-Sep-1999 #sequence_revision 0.; Hirt, H.; Scheel, D.
Science 276, 2054-2057, 1997
A;Title: Receptor-mediated activation of a MAP kinase in pathogen defense of plants.
A;Reference number: Z18265; MUID:97342856; PMID:9197271
                                                                                                                                                                                                                                                                                                                                                                     80 AMNSETNESVAIKKIANAFDNKIDAKRTIREIKULRHMDHENIVAIRDIIPPPPLRNAFND 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200 NCDLKICDFGLARVISESDFWIEYVVTRWYRAPBLLLLNSSDYTAAIDVWSVGCIFWBLMD 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     319 PLAIDLIEKMLTFDPRRRITYLDALAHPYLNSLHDISDEPECTIPFNFDFENHALSEEQM 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 IRSNOELSEEHCOYFLYQILRGLKYIHSANVIHRDLKPSNLLLNANCDLKICDFGLARPS 187
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                                                                                                                                                                                                                                          20 GPPAAAPSPQMPGIENIPATLSHGGRFIQYNIFGNIFEVTAKYKPPIMPIGKGAYGIVCS
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                                                                                                                                    45;
                                                                    2,
                                                                Score 1442; DB 2;
Pred. No. 2.8e-53;
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A;Molecule type: mRNA
   F;69-77/Region: protein kinase ATP-binding motif
                                                                                                                                    46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56; Mismatches
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72.1%;
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379 KELIYREALAFNP 391
                                                             Query Match
Best Local Similarity 72.41
Matches 270; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mitogen-activated protein kinase 6 (EC 2.7.1.-) - Arabidopsis thaliana
NyAlternate names: MAP kinase (ATMPK6)
CiSpecies: Arabidopsis thaliana (mouse-ear cress)
CiSpecies: Arabidopsis thaliana (mouse-ear cress)
CiDate: 06-Oct-1994 sequence_revision 19-Jan-1996 #text_change 09-Jul-2004
CiAccession: 840472; E84870
Rimizoguchi T.; Hayashida, N.; Yamaguchi-Shinozaki, K.; Kamada, H.; Shinozaki, K.
FEBS Lett. 336, 440-444, 1993
A;Title: ATMPK8: a gene family of plant MAP kinases in Arabidopsis thaliana.
A;Reference number: 840469; MUID:94109583; PMID:8282107
A;Andlecule type: mRNA
A;Residues: 1-395 «MIZ>
A;Coss-references: UNIPROT:Q39026; UNIPARC:UPIO0000014BF; EMBL:D21842; NID:9457403; PIL
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shen, M.; Vanaken, S.B.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nittle: All-768, 1999
Nature 402, 761-768, 1999
   PII
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UNIPROT: Q40532; UNIPARC: UPI0000130582; EMBL: X83880; NID: 9634069;
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A.Reference number: A64420; MUD:20083487; PMID:10617197
A.Reference number: A64420; MUD:20083487; PMID:10617197
A.Reference number: A64420; MUD:200834870
A.Residues: DNA
A.Residues: 1-395 <STO>
A.Residues: 1-395 <STO
A.Residues: 1-395 <
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C)Genetics:
A)Gene: ntf4
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Scywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;57-345/Domain: protein kinase homology <KIN>
F;66-74/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                     PVAGIDNIPATLSHGGRFIQYNIFGNIFEVTAKYKPPIMPIGKGAYGIVCSALNSETNEH
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                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                     Length 393;
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                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                               44;
                                                                                                                                                                                                                                                               74.0%; Score 1445.5; Di
72.6%; Pred. No. 2e-53;
tive 52; Mismatches
                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 72.64
Matches 267; Conservative
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130

127

70

67

Gaps

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Length 371;

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A;Molecule type: mRNA
A;Residues: 1-371 <WI2>
A;Cross-references: UNIPROT:Q40531; UNIPARC:UPI0000130583; EMBL:X83879; NID:g634067; PID
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,MOlecule type: mRNA
A,Reaidues: 1-213,'D',215-371 <JOW>
A,Cross-references: UNIPARC:UP1000012F26D; EMBL:X82268; NID:g1204128; PIDN:CAAS7719.1; F
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                                                                                                                       A,Gene: ntf6
C,Superfamily: kinase-related transforming protein; protein kinase homology
C,Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F,35-324/Domain: protein kinase homology <KIN>
F,44-52/Region: protein kinase ATP-binding motif
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mitogen-activated protein kinase MMK2 (EC 2.7.1.-) - alfalfa
C;Species: Medicago sativa (alfalfa)
C;Dacession: S60121; S69551
R;Jonak, C.; Kiegerl, S.; Lloyd, C.; Chan, J.; Hirt, H.
MOI. Gen. Genet. 248, 686-694, 1995
A;Fitle: MMK2, a novel alfalfa MAP kinase, specifically complements the yease
A;Feference number: S60121; MUID:96069707; PMID:7476871
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 ANAFINDMDAKRTLREIKLLRHLDHENIIGIRDVIPPPIPQAFNDVYIATELMDTDLHHI
                                                                                                                                                                                                                                                                                                                                                                  8 BFRPTWTHGGRYLLYDIFGNKFEVTNKYQPPIMPIGRGAYGIVCSVMNFETREMVAIKKI
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                                                                                                                                                                                                                                                                   Length 371;
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A;Residues: 1-371 <JON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q40353; UNIPARC:UPI0000175591
R;Jonak, C.
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                                                                                                                                                                                                                                                                   ; Score 1327.5; DB 2;
; Pred. No. 1.4e-48;
59; Mismatches 59;
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                                                                                                                                                                                                                                                                      68.0%; Score 1327.5; 66.9%; Pred. No. 1.4e
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Matches 240; Conservative
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A, Reference number: S69551
A, Accession: S69551
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833635
mitogen-activated protein kinase homolog (clone D5) - garden pea
NiAlternate names: MAP kinase homolog
C; Species: Pisum sativum (garden pea)
C; Species: Pisum sativum (garden pea)
C; Species: Disum sativum (garden pea)
C; Stafstrom; J.P.; Altechuler, M.; Anderson, D.H.
C; Accession: S33635; S31836
R; Stafstrom, J.P.; Altechuler, M.; Anderson, D.H.
Plant Mol. Biol. 22, 83-90, 1993
A; Title: Molecular cloning and expression of a MAP kinase homologue from pea.
A; Reference number: S33635; MUID:93271463; PMID:8388749
A; Accession: S33635
A; Molecule type: mRNA
A; Residues: 1-394 ASTA,
A; Cross-references: UNIPROT:Q06060; UNIPARC:UPI000012EBC5; EMBL:X70703; NID:g20807; PIDN
C; Superfamily: Kinase-related transforming protein; protein kinase homology
C; Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k
F; 59-347/Domain: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    uitogen-activated protein kinase 6 (EC 2.7.1.-) - common tobacco
MyAlternate names: serine/threonine-specific protein kinase p43Ntf6
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: 868189; S31320
Bir. J. Biochem. 233, 249-257, 1995
Bur. J. Biochem. 233, 249-257, 1995
A;Title: Molecular cloning, functional expression in Escherichia coli, and characterizat A;Reference number: 868189; MUID:96061956; PMID:7588752
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                                                                                                   LITEVIGTPTDDELGFIRNEDARKYMRHLPQYPRRTFASMFPRVQPAALDLIERMLTFNP 306
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                                                                                                                                                                                                  307 LORITVEEALDHPYLERLHDIADEPICLEPFSFDFEQKALNEDOMKOLIFNEAIEMNPN 365
                                                                                                                                                                                                                           SKRITVEEALAHPYLARLHDIADEPICTKPFSFEFRTAHLGERQIKOMIYQEALAFNPD 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               192 MATEYVVTRWYRAPELLLINSTDYSAA-DVWSVGCIFWELINRQPLFPGRDHMHQMRLITE
                           TDDBPMTEYVVTRWYRAPELLINSSDYTVAIDVWSVGCIYMELMNRKPLFAGKDHVHQMR
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LLTELLGSPTEADLGFVRNEDAKRPILQLPRHPRQPLRQLYPQVHPLAIDLIDKMLTFDP
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262; Conservative
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RESULT 13

Micogen-activated protein kinase 4 (EC 2.7.1.-) - Arabidopsis thaliana
Nilecrate names: MAP kinase
C; Accession: Arabidopsis thaliana (mouse-ear cress)
C; Accession: Standardopsis thaliana
C; Accession: Standardopsis thaliana
N; C; Accession: Standardopsis thaliana
N; C; Accession: Standardopsis thaliana
N; C; Accession: T01707
N; Accession: T01707
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                                                                                     SNQPWTDDHCRYFVYQLLRGLKYVHSANVLHRDLKPSNLLLNANCDLKIGDFGLARTTSE 190
                                                                                                                                                                                                                                  SDMMTEYVVTRWYRAPELLLINSTDYSAA-DVWSVGCIFMELINRQPLFPGRDHMHQMRLI 248
                                                                                                                                                                                                                                                          TEVIGTPTDDELGFIRNEDARKYMRHLPQYPRRTPASMFPRVQPAALDLIERMLTFNPLQ 308
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                                                                                                                                               SNQELSEEHCQYFLYQILRGLKYIHSANVIHRDLKPSNLLLNANCDLKICDFGLARPSSE
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66.2%; Pred. No. 4.4e-48;
ive 62; Mismatches 56; Indels
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Matches 233; Conservative
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Cibate: Oz-Mar-Zo01 #sequence_revision 02-Mar-Zo01 #text_change 09-Jul-Zo04
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Cipate: OZ-Mar-Zo01 #sequence_revision 02-Mar-Zo01 #text_change 09-Jul-Zo04
CiAccession: C86146
CiAccession: C86146
Cirin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; aneen, N.R.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Liu, X.X.; Liu, Z.A.; Lucos, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Mu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Attle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: C86146
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C; Genetics:
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DMDAKRTLREIKLLRHLDHENIIGIRDVIPPPIPQAFNDVYIATELMDTDLHHIIRSNQE 133
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                                 261 GSPDDSSLGFLRSDNARRYVRQLPQYPRQNFAARPPNMSAGAVDLLEKMLVFEPSRRITV
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C;Superfamily: kinase-related transforming protein; protein kinase homology
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                                                                                                                                                                                                                                                     TEYVVTRWYRAPELLINSTDYSAA-DVWSVGCIFMELINRQPLFPGRDHMHQMRLITEVI
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llarity 64.6%; Pred. No. 1.6e-46;
Conservative 64; Mismatches 61; Indels 1;
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mitogen-activated protein kinase 5 (EC 2.7.1..) - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Daccession: 340471
R;Mizoguchi, T.; Hayashida, N.; Yamaguchi-Shinozaki, K.; Kamada, H.; Shinozaki, K.
FBES Lett. 336, 440-444, 193
A;Title: ArMPKs: a gene family of plant MAP kinases in Arabidopsis thaliana.
A;Reference number: 840469; MUID:94109583; PMID:8282107
A;Residues: 1-376 cMIZ>
A;Residues: 1-376 cMIZ>
A;Residues: 1-376 cMIZ>
A;Cossasion: S40471
A;Molecule type: mRNA
A;Residues: 1-376 cMIZ>
A;Cossasion: Superfamily: kinase-related transforming protein; protein kinase homology
C;Genetics:
A;Gene: MPKS
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;40-238/Domain: protein kinase ATP-binding motif
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 NDMDAKRTLREIKLLRHLDHENIIGIRDVIPPPIPQAFNDVYIATELMDTDLHHIIRSNQ 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 MTHGGRYLLYDIFGNKFEVTNKYQPPIMPIGRGAYGIVCSVMNFETREMVAIKKIANAFN 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 LVHGGRYFQYNVYGNLFEVSNKYVPPIRPIGRGAYGFVCPAVDSETHEEIAIKKIGKAFD 79
IGTPIDDELGFIRNEDARKYMRHLPQYPRRIFASMFPRVQPAALDLIERMLTFNPLQRIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 64.4%; Score 1257.5; DB 2; Length 376; Best Local Similarity 63.7%; Pred. No. 1.1e-45; Matches 225; Conservative 66; Mismatches 61; Indels 1;
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Search completed: December 27, 2005, 20:41:08 Job time : 41 secs

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December 27, 2005, 20:20:31; Search time 188 Seconds (without alignments) 860.061 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                        - protein search, using sw model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Adt02330 Rice mito	Aag34157 Zea mays							Aag31653 Arabidops			Aab48047 Signal tr		Adx79753 Plant ful	Adt02332 Rice mito	Adyl1673 Plant ful	Aag33123 Zea mays		Adyl1385 Plant ful	Aag33124 Zea mays	Aag04672 Arabidops	-		Aag30672 Arabidops
SUMMARIES	ΩI	ADT02330	AAG34157	AAB48046	AAG34158	AAG34159	AAW15512	AAB48048	AAG31654	AAG31653	AAG31655	AAW61252	AAB48047	AAW15513	ADX79753	ADT02332	ADY11673	AAG33123	AAB48044	ADY11385	AAG33124	AAG04672	AAG45420	ADT60480	AAG30672
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مد	Query Match	100.0	92.3	92.1	83.6	79.7	75.4	74.2	73.8	73.8	73.8	73.7	72.9	7.07	9.89	68.3	68.2	67.9	67.9	67.9	9.79	67.4	65.5	63.1	63.0
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Aag42613 Arabidops	Aag42612 Arabidops	Aag06702 Arabidops	Aag06701 Arabidops	Aag30978 Arabidops		Adx73133 Plant ful	Aag04673 Arabidops		Aag44681 Zea mays	Aag44680 Zea mays		Abm74137 DNA clone	Aab48043 Signal tr			Aag44792 Zea mays	Aag35746 Zea mays	Aag44791 Zea mays		Aab48045 Signal tr
AAG42613	AAG42612	AAG06702	AAG06701	AAG30978	AAM52837	ADX73133	AAG04673	AAG33125	AAG44681	AAG44680	AAG44679	ABM74137	AAB48043	ADT60889	AAG44793	AAG44792	AAG35746	AAG44791	AAG35745	AAB48045
372 3	406 3	372 3	379 3	354 3	311 5	216 8	280 3	280 3	366 3	367 3	369 3	369 7	369 4	370 8	367 3	368 3	368 3	370 3	370 3	370 4
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## ALIGNMENTS

Rice; mitogen-activated protein kinase 5a; MAPK5; MAPK5a; abiotic stress tolerance; biotic stress tolerance; drought; temperature; salinity; plant; enzyme. Rice mitogen-activated protein kinase 5a (MAPK5a) polypeptide. /note= "Encoded by ATCGAC" Location/Qualifiers ADT02330 standard; protein; 368 AA. 31-JAN-2004; 2004US-00768886. 31-JAN-2003; 2003US-0444249P (first entry) WPI; 2004-747214/73. Misc-difference 218 Yang Y, Xiong L; (YANG/) YANG Y. (XION/) XIONG L. N-PSDB; ADT02329 US2004209325-A1. Oryza sativa, 13-JAN-2005 21-OCT-2004. ADT02330; RESULT 1 ADT02330 

New isolated nucleic acid molecule encoding a mitogen-activated protein kinase-5 (MAPKS) polypeptide, useful for increasing tolerance to abiotic and biotic stress in plants. Claim 24; SEQ ID NO 2; 36pp; English. The invention relates to a rice mitogen-activated protein kinase 5 (MAPKS) polypeptides and the polymucleotides encoding them. The invention also relates to an antibody that specifically binds to a peptide consisting of a C-terminal portion of a MAPKS polypeptide, a transgenic plant transformed by a polymucleotide encoding a MAPKS orthologue where

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9905-0140351P-
9905-0140354P-
9905-0140951P-
9905-0140991P-
9905-0141842P-
9905-014287P-
9905-0142184P-
9905-0142390P-
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04-MAY-1999;
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11-MAY-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
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16-APR-1999;
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  over expression of the MAPKS orthologue in the plant results in increased for lecrance to abiotic stress compared to a wild-type plant and a method for evaluating a plant for tolerance to abiotic stress comprising treating a plant with abiotic stress, isolating a MAPKS protein from the plant, detecting MAPKS activity and evaluating the increase or decrease indicates the plant where the increase in MAPKS activity in the plant where the increase in MAPKS activity indicates the plant are useful for increasing tolerance compositions of the present invention are useful for increasing tolerance to abiotic and blotic stress in plants using MAPKS, where the abiotic stress is decought, temperature or salinity and the biotic stress is from pathogenic bacteria, viruses, nematodes and insects. This sequence represents the rice MAPKSa polypeptide of the invention.
                                                                                                                                                                                                                                                                                    120
                                                                                                                                                                                                                                                                                                 61 MVAIKKIANAFNNDMDAKRTLREIKULRHLDHENIIGIRDVIPPPIPQAFNDVYIATELM 120
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                                                                                                                                                                                                                                                  1 MDGAPVAEFRPTMTHGGRYLLYDIFGNKFEVTNKYQPPIMPIGRGAYGIVCSVMNFETRE
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                                                                                                                                                                                     Length 368;
                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                  100.0%; Score 1953; DB 8;
100.0%; Pred. No. 8.5e-192;
rative 0; Mismatches 0;
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99US-0123180P.
99US-0123548P.
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                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 368; Conservative
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EMNPNIRY 368
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05-MAR-1999;
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RR 19-JUL-1999 9905-0144332P
RR 20-JUL-1999 9905-0144332P
RR 21-JUL-1999 9905-0144332P
RR 21-JUL-1999 9905-0144332P
RR 21-JUL-1999 9905-0144332P
RR 22-JUL-1999 9905-0144632P
RR 22-JUL-1999 9905-0144632P
RR 23-JUL-1999 9905-014508P
RR 23-JUL-1999 9905-014508P
RR 23-JUL-1999 9905-014508P
RR 23-JUL-1999 9905-014532P
RR 02-AUG-1999 9905-014732P
RR 02-AUG-1999 9905-014732P
RR 13-AUG-1999 9905-014732P
RR 13-AUG-1999 9905-014732P
RR 13-AUG-1999 9905-014732P
RR 23-AUG-1999 9905-014732P
RR 23-AUG-1999 9905-014732P
RR 23-AUG-1999 9905-014932P
RR 23-AUG-1999 9905-014933P
RR 23-AUG-1999 9905-015308P
RR 23-AUG-1999 990
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RMLTENPLOR ITVEEALDHPYLERLHDIADEPICLEPFSFDFEQKALNEDQMKQLIFNEA
                                                                                                                                                                                                                                                                                                 FGLARPSSESDMMTEYVVTRWYRAPELLINSTDYSAA-DVWSVGCIFMELINRQPLFPGR
                                                                                                                                                                                                                                                                                                                                                                                                          DHMHOMRLITEVIGTPTDDELGFIRNEDARKYMRHLPQYPRRTFASMFPRVQPAALDLIE
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
92.3%; Score 1803.5; DB 3; Length 374;
Best Local Similarity 91.3%; Pred. No. 2.1e-176;
Matches 337; Conservative 18; Mismatches 13; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB48046 standard; protein; 374
9905-0158029P.
9905-0158232P.
9905-0158234P.
9905-0159294P.
9905-0159294P.
9905-0159330P.
9905-0159331P.
9905-0159637P.
9905-0159631P.
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RMLTFNPLQRITVEEALDHPYLERLHDIADEPICLEPFSFDFEQKALNEDQMKQLIFNEA 359
                               Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
                                                                                                                                                                                                                                                                                                               Zea mays protein fragment SEQ ID NO: 41519.
                                                                                                                                                                                                          AAG34158 standard; protein; 330 AA.
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99US-0132407P.
99US-0132484P.
99US-0132485P.
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99US-0132487P.
99US-0132863P.
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99US-0135629P.
99US-0136021P.
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99US-0123548P.
99US-0125788P.
99US-0126264P.
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99US-0127462P.
99US-0128234P.
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99US-0129845P.
99US-0130077P.
99US-0130449P.
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99US-0130891P.
99US-0131449P.
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99US-0138094P.
99US-0138540P.
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                                                                                                                                                                                                                                                                              18-OCT-2000 (first entry)
                                                                                                                   366 MELNPNFRY 374
                                                                                  360 IEMNPNIRY 368
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18-MAY-1999;
19-MAY-1999;
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19-APR-1999;
21-APR-1999;
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23-APR-1999;
28-APR-1999;
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08-APR-1999;
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30-APR-1999;
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05-MAY-1999;
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06-MAY-1999;
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14-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FGLARPSSESDMMTEYVVTRWYRAPELLLMSTDYSAA-DVWSVGCIFMELINRQPLFPGR 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 MVAIKKIANAPDNHMDAKRTLRBIKLLRHLDHENIIGIRDVIPPPVPQAFNDVYIGTELM 125
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                                                                                                                                                                                                                                                                                                                                                                                                     New signal transduction nucleic acids and encoded proteins useful for regulating phychoramone expression, including ethylene, auxins, cytokinins and gibberellin, to provide control of plant response to environmental stresses.
                             Zea mays; maize; signal transduction protein; phytohormone; ethylene; auxin; cytokinin; gibberellin; immunogen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 13; Page 91; 126pp; English.
                                                                                                                                                                                                                                                                                (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                           99US-0142996P.
                                                                                                                                                                                          28-APR-2000; 2000WO-US011687
                                                                                                                                                                                                                           99US-0134292P
Signal transduction protein.
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Best Local Similarity 90.8
Matches 335; Conservative
                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-031929/04.
                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAC84259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 374 AA;
                                                                                                                    WO200070059-A2.
                                                                                                                                                                                                                                                                                                                  Helentjaris TG;
                                                                                                                                                                                                                             14-MAY-1999;
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| 90S - 014817<br>90S - 014831<br>90S - 014834<br>90S - 014836<br>90S - 014936<br>90S - 014936<br>90S - 014972<br>90S - 014972<br>90S - 014972<br>90S - 014972<br>90S - 014972<br>90S - 014936<br>90S - 014936<br>90 | 90% - 0.15.106 90% - 0.15.106 90% - 0.15.106 90% - 0.15.130 90% - 0.15.130 90% - 0.15.236 90% - 0.15.236 90% - 0.15.240 90% - 0.15.240 90% - 0.15.240 90% - 0.15.240 90% - 0.15.240 90% - 0.15.240 90% - 0.15.240 90% - 0.15.240 90% - 0.15.240 90% - 0.15.240 90% - 0.15.240 90% - 0.15.240 90% - 0.15.240 90% - 0.15.240 90% - 0.15.240 90% - 0.15.240 90% - 0.15.240 90% - 0.15.240 90% - 0.15.240 90% - 0.15.240 90% - 0.15.240 90% - 0.15.240 90% - 0.15.240 90% - 0.15.240 | \$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\text{State}\$\tex |  |
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          |  |

Query Match
Best Local Similarity 93.0%; Pred. No. 7.1e-159;
Matches 307; Conservative 12; Mismatches 10; Indels 1; Gaps

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990S-0139458P.
990S-0139460P.
990S-0139461P.
990S-0139462P.
990S-0139463P.
990S-0139750P.
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       9905-0135124P

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990S-0145224P-
990S-0145216P-
990S-0145913P-
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24-JUN-1999;
28-JUN-1999;
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15.70L-1999;
16.70L-1999;
19.70L-1999;
19.70L-1999;
19.70L-1999;
19-MAY-1999;
20-MAY-1999;
24-MAY-1999;
25-MAY-1999;
25-MAY-1999;
28-MAY-1999;
01-JUN-1999;
04-JUN-1999;
                                                                                07-JUN-1999;
08-JUN-1999;
10-JUN-1999;
10-JUN-1999;
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18-JUN-1999;
18-JUN-1999;
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HRDLKPSNLLLNANCDLKICDFGLARPSSESDMMTRYVVTRWYRAPELLLNSTDYSAA-D 218
                                                                                                   240
                                                                                                                 PRRTFASMFPRVQPAALDLIERMLTFNPLQRITVEBALDHPYLERLHDIADEPICLEPFS 338
                                                                                                                                                                                                                                                                              Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
MPIGRGAYGIVCSVMNSETKEMVAIKKIANAPDNHMDAKRTLREIKLLRHLDHENIIGIR
                                                                                          181 VWSVGCIFMELINRQPLFPGRDHMHQMRLITEVIGTPTDDELGFIRNEDARKYWRHLPQF
                 DVIPPPIPQAPNDVYIATELMDTDLHHIIRSNQELSEEHCQYFLYQILRGLKYIHSANVI
                                                                                  VWSVGCI FMELINRQPLFPGRDHWHQMRLITEVIGTPTDDELGFIRNEDARKYMRHLPQY
                         PDFEOKALNEDOMKOLIFNEAIEMNPNIRY 368
                                                                                                                                                                                                                                                              Zea mays protein fragment SEQ ID NO: 41520.
                                                                                                                                                                                                             AAG34159 standard; protein; 316 AA
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990S-0123548P

990S-0125788P

990S-0126782P

990S-0127462P

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990S-0128714P

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990S-0130819P

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990S-0134219P.
990S-0134221P.
990S-0134370P.
990S-0134768P.
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                                                                                                                                                                                                                                              18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                Zea mays subsp. mays
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09-MAR-1999)

23-MAR-1999)

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06-MAY-1999)

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06-MAY-1999;
07-MAY-1999;
11-MAY-1999;
14-MAY-1999;
14-MAY-1999;
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RR 04-AUG-1999 99US-014536P.

RR 04-AUG-1999 99US-014536P.

RR 04-AUG-1999 99US-014730EP.

RR 05-AUG-1999 99US-014730EP.

RR 11-AUG-1999 99US-014730EP.

RR 11-AUG-1999 99US-01433EP.

RR 11-AUG-1999 99US-01433EP.

RR 11-AUG-1999 99US-01435EP.

RR 11-AUG-1999 99US-01435EP.

RR 11-AUG-1999 99US-01492EP.

RR 11-AUG-1999 99US-01493EP.

RR 11-AUG-1999 99US-01493EP.

RR 20-AUG-1999 99US-01493EP.

RR 21-AUG-1999 99US-01493EP.

RR 22-AUG-1999 99US-01493EP.

RR 22-AUG-1999 99US-01493EP.

RR 22-AUG-1999 99US-01436EP.

RR 23-AUG-1999 99US-01536EP.

RR 23-AUG-1999 99US-015310P.

RR 23-AUG-1999 99US-0153294P.

RR 23
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113
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                                                                                                                                                                                                                                                                              292
                                                                                                                                                                                                                                                                                                                             293 AALDLIERMLTFNPLQRITVEEALDHPYLERLHDIADEPICLEPFSFDFEQKALNEDQMK 352
                                                                                                                                                                                                                                                                                                                                          241 VALDLIERMLTFNPLQRITVEBALEHPYLERLHDVADEPICTDPFSFDFEQQALTEDQMK 300
                                                                                                                                                                                 173
                                                                                                                                                                                                                               232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW15512 and AAW15513 represent the mitogen activated protein (MAP) kinases of the invention. This sequence contains the T-E-Y sequence, in which the threonine and tyrosine residues are phosphorylated to activate the protein at residues201-203. The MAP kinase and its gene can be used
                                                                                                                                  QPLFPGRDHMHQMRLITEVIGTPTDDELGFIRNEDARKYMRHLPQYPRRTFASMFPRVQP
                                                                                                                                                                                 114 YIATELMDTDLHHIIRSNQELSEEHCQYFLYQILRGLKYIHSANVIHRDLKPSNLLLNAN
                                                                                                                                                                                                                                 CDLKI CDFGLARPSSESDMMTEYVVTRWYRAPELLLINSTDYSAA-DVWSVGCI FMELINR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wound-stress inducible MAP kinase - used to regulate the synthesis of
                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mitogen activated protein kinase; MAP; infectious specific protein; plant; jasmone acid.
                                                                                                           ;
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                                                                                     DB 3; Length 316;
                                                                                 Query Match
Pest Local Similarity 92.7%; Pred. No. 3.5e-151;
Matches 293; Conservative 12; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW15512 standard; protein; 375 AA.
99US-0161360P.
99US-0161361P.
99US-0161920P.
99US-0161992P.
99US-016193P.
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N-PSDB; AAT60349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAP kinase #1
 26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                         LTFNPLQRITVERALDHPYLERLHDIADEPICLEPFSFDFEQKALNEDQMKQLIFNEAIE 361
                                                                                                                                                62
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to regulate the synthesis of jasmone acid and the synthesis of a group o infectious specific proteins. By introducing the MAP kinase gene into a plant, thereby inducing expression of the mRNA for MAP kinase (or its antisense RNA), the synthesis of jasmone acid and a group of infectious specific proteins can be regulated in the plant
                                                                                                                                                             GGQFPDFPSVLTHGGQYVQFDIFGNPFEITTKYRPPIMPIGRGAYGIVCSVLNTELNEMV
                                                                                                                                                                                              AIKKIANAPNNDMDAKRTLREIKLLRHLDHENIIGIRDVIPPPIPQAFNDVYIATELMDT
                                                                                                                                                                                                            DLHHIRSNQELSEEHCQYFLYQILRGLKYIHSANVIHRDLKPSNLLLNANCDLKICDFG
                                                                                                                                                                                                                                                         DLHQIIRSNQGLSEDHCQYFWYQLLRGLKYIHSANVLHRDLKPSNLLVNANCDLKICDFG
                                                                                                                                                                                                                                                                                                       GAPVAEFRPTMTHGGRYLLYDIFGNKFEVTNKYQPPIMPIGRGAYGIVCSVMNFETREMV
                                                                                                                                                                                                                                                                                           LARPSSESDMMTEYVVTRWYRAPELLLNSTDYSAA-DVWSVGCIFMELINRQPLFPGRDH
                                                                                                                                                                                                                                                                                                                                         MHQMRLITEVIGTPTDDELGFIRNEDARKYMRHLPQYPRRTFASMFPRVQPAALDLIERM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      signal transduction protein; phytohormone; ethylene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New signal transduction nucleic acids and encoded proteins useful for
                                                                                                                          Gapa
                                                                                                                         ;
                                                                                                 DB 2; Length 375;
                                                                                                                       Indels
                                                                                                                        41;
                                                                                               75.4%; Score 1472.5; DB 2
72.5%; Pred. No. 2.5e-142;
tive 58; Mismatches 41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB48048 standard; protein; 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transduction protein.
                                                                                                           Best Local Similarity 72.5%
Matches 263; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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N-PSDB; AAC84265.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         maize;
                                                                         Sequence 375 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                       MNP 364
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08-JUL-1999;
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The invention provides Zea mays signal transduction proteins and encoding nucleotide sequences. The nucleic acids are useful for requiating connected sequences. The nucleic acids are useful for requiating of phytohormones, including ethylene, auxins, cytokinins, and gibberellin, to effect developmental changes in plants and provide control of plant response to environmental stresses. They may also be control of plant response to environmental stresses. They may also be control of gene transcripts, for detecting mutations in the gene, for solation of gene transcripts, for detecting mutations in the gene, for controling upregulation of expression or changes in enzyme activity in screening assays of compounds, for detection of any number of allelic contributer be used for recombinant expression of their encoded polypeptides, as immunogens in the preparation or screening of antibodies, and in sense contains may be used in assays for enzyme agonists or antagonists, as immunoreactive with the proteins. The present sequence represents a signal transduction contains of the invention contains and antibodies specifically immunoreactive contains of the invention contains and antibodies as a signal transduction contains and antibodies and antibod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 VAIKKIANAFDNKIDAKRILKILRHMDHENIVAIRDIIPPPLREAFNDVYIAYELMD 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
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  phytohormone expression, including ethylene, and gibberellin, to provide control of plant
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ive 51; Mismatches 43;
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113 VYIATELMDTDLHHIIRSNQELSEEHCQYFLYQILRGLKYIHSANVIHRDLKPSNLLLNA 172 GAPVAEFRP-----TWTHGGRYLLYDIFGNKFBYTNKYQPPIMPIGRGAYGIVCS Gaps 12; / Match 73.8%; Score 1442; DB 3; Length 395; Local Similarity 72.4%; Pred. No. 3.7e-139; nes 270; Conservative 46; Mismatches 45; Indels 1 9908-0149926P.
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9908-0149923P.
9908-0149923P.
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27-AUG-1999;
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9905-0144632P
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 140 VYIAYELMDTDLHQIIRSNQALSEEHCQYFLYQILRGLKYIHSANVLHRDLKPSNLLLNA 199
                              231
                                                259
                                                                    291
                                                                            PAALDLIERMLTFNPLORITVEEALDHPYLERLHDIADEPICLEPFSFDFEQKALNEDOM 351
                                                                                                                                                                                                                                                                                           Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                           ROPLFPGRDHMHOMRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMFPRVO
                                                                                                                                                                                                                                                                          Arabidopsis thaliana protein fragment SEQ ID NO: 38050.
                                                                                                                                                                                                                   AAG31655 standard; protein; 366 AA.
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99US-0123480P

99US-012548BP

99US-01264P

99US-01264P

99US-01262BP

99US-0128234P

99US-0128234P

99US-0130814P

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990S-0135124P.
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                                                                                                                                                KOLIFNEAIEMNP 364
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KELIYREALAFNP 391
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                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana
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09-MAR-1999

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RR 03-AUG-1999; 99US-0147304P.
RR 04-AUG-1999; 99US-0147304P.
RR 05-AUG-1999; 99US-0147304P.
RR 05-AUG-1999; 99US-0147302P.
RR 05-AUG-1999; 99US-0147302P.
RR 10-AUG-1999; 99US-0147310P.
RR 11-AUG-1999; 99US-014731P.
RR 11-AUG-1999; 99US-0148314P.
RR 11-AUG-1999; 99US-0148314P.
RR 11-AUG-1999; 99US-0148314P.
RR 11-AUG-1999; 99US-0148314P.
RR 11-AUG-1999; 99US-014932P.
RR 21-AUG-1999; 99US-011066EP.
RR 21-AUG-1999; 99US-011066EP.
RR 21-AUG-1999; 99US-01106EP.
RR 21-AUG-1999; 99US-0110912P.
RR 21-AUG-1999; 99US-0110913P.
RR 21-AUG-1999; 99US-0110919P.
RR 21-AUG-1999; 99US-011
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250
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                                                                                                                                                                                                                                                                   251 VIGTPTDDELGFIRNEDARKYMRHLPQYPRRTFASMPPRVQPAALDLIERMLTFNPLQRI 310
                                                                                                                                131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This represents a salicylic acid induced protein (SIP) kinase. This SIP kinase is an unique member of the mitogen-activated protein (MAP) kinase family. The salicylic acid induced MAP kinase of the invention comprises
                                                                                                          69
                                                                                                                                                                                                                      72 NNDMDAKRTLREIKLLRHLDHENIIGIRDVIPPPIPQAFNDVYIATELMDTDLHHIIRSN
                                                                                                                                            QELSBEHCQYFLYQILRGLKYIHSANVIHRDLKPSNLLLLNANCDLKICDFGLARPSSESD
                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salicylic acid induced protein; SIP; mitogen-activated protein; MAP; tobacco; disease resistance; microbial pathogen; MAP kinase.
                                                                                                                                                                                                                                                                                                              TVEEALDHPYLERLHDIADEPICLEPFSFDFEQKALNEDQMKQLIFNEAIEMNP 364
                                                                                                                                                                                                                                                                                                                           Salicylic acid induced MAP kinase - obtained from tobacco, used to produce plants having increased disease resistance, against e.g. microbial pathogens.
                                                                5
                                          Length 366;
                                                                Indels
                                         Query Match 73.8%; Score 1441; DB 3; Best Local Similarity 75.1%; Pred. No. 4.2e-139; Matches 266; Conservative 46; Mismatches 40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 28; Page 62-63; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                           AAW61252 standard; protein; 393 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salicylic acid induced MAP kinase.
99US-0161992P.
99US-0161993P.
99US-0162142P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97WO-US019219
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97US-00837593
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                                 Query Match
Focal Similarity
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28-OCT-1999;
28-OCT-1999;
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21-APR-1997;
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AAW61252
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activated by an agent that induces a disease defence response in plants depway of a signal transduction pathway that is at least partially dependent on salicylic acid. Host plant cells transformed with a vector containing a recombinant DNA molecule encoding the salicylic acid induced MAP kinase is used to produce the protein recombinantly. The products can be used to produce plants with increased disease resistance. The products may also be used as a research tool to identify other proteins involved in the hypersensitive response and systemic acquired response in plants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84
                                                                                                                                                                                                                                         DTDLHQIIRSNQGLSEEHCQYFLYQILRGLKYIHSANVLHRDLKPSNLLLNANCDLKICD
                                                                                                                                                                                                                                                                                                                                                                                                            DHMHQMRLITEVIGTPTDDELGFIRNEDARKYMRHLPQYPRRTFASMFPRVQPAALDLIE
                                                                                                                                                                                                                          1 MDGAPVAEFRPTWTHGGRYLLYDIFGNKFEVTNKYQPPIMPIGRGAYGIVCSVMNFETRE
                                                                                                                                                                                                                                                                                                                                     DTDLHHIIRSNQELSEEHCQYFLYQILRGLKYIHSANVIHRDLKPSNLLLNANCDLKICD
                                                                                                                                                                                                                                                                                                                                                                                            FGLARPSSESDMMTEYVVTRWYRAPELLLNSTDYSAA-DVWSVGC1FMELINRQPLFPGR
 The protein is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zea mays; maize; signal transduction protein; phytohormone; ethylene; auxin; cytokinin; gibberellin; immunogen.
                                                                                                                                                                   DB 2; Length 393;
serine/threonine kinases.
                                                                                                                                                                                                45;
                                                                                                                                                                  73.7%; Score 1438.5; DB 2, 72.4%; Pred. No. 8.5e-139; ive 50; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB48047 standard; protein; 398 AA.
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99US-0142996P.
 subdomains I to XI of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal transduction protein.
                                                                                                                                                                               Local Similarity 72.41 es 267; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IEMNPNIRY 368
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LAFNPEYQH
                                                                                                                                         Sequence 393 AA;
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08-JUL-1999;
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Matches
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The invention provides Zea mays signal transduction proteins and encoding nucleotide sequences. The mucleic acids are useful for regulating expression of phytohormones, including ethylene, auxins, cytokinins, and cibberellin, to effect developmental changes in plants and provide control of plant response to environmental stresses. They may also be control of plant response to environmental stresses. They may also be control of plant response to environmental stresses. They may also be control of gene transcripts, for detecting mutations in the gene, for monitoring upregulation of expression or changes in enzyme activity in strength or for site-directed mutagenesis in enzyme activity in variants, or for site-directed mutagenesis in enkaryotic cells. They may further be used for recombinant expression of their encoded polypeptides, as immunogens in the preparation or screening of antibodies, and in sense or antisense suppression of genes in a host cell, tissue or plant. The proteins may be used in assays for enzyme agonists or antagonists, as immunogens or antisense to obtain antibodies specifically immunoreactive with the proteins. The present sequence represents a signal transduction protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94 AIKKIANAFDNKIDAKRTLREIKLLRHMDHENIVAIRGIIPPAQRAAFNDVYIAYELMDT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LTFNPLQRITVEEALDHPYLERLHDIADEPICLEPFSFDFEQKALNEDQMKQLIFNEAIE 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154 DLHQIIRSNQALSEEHCQYFLYQILRGLKYIHSANVLHRDLKPSNLLLNANCDLKICDFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           214 LARTISETDFWIEVVVIRWYRAPELLINSSEYTAAIDVWSVGCIFWELMDRKPLFPGRDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DLHHI IRSNQELSEEHCQYFLYQI LRGLKYI HSANVI HRDLKPSNLLLNANCDLKI CDFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LARPSSESDMMTEYVVTRWYRAPELLLNSTDYSAA-DVWSVGCIFMELINRQPLFPGRDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 GVMLDNIQATLSHGGRFIQYNIFGNVFEVTAKYKPPVLPIGKGAYGIVCSALNSETAEQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AIKKIANAFNNDMDAKRTLREIKLLRHLDHENIIGIRDVIPPPIPQAFNDVYIATELMDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAPVAEFRPTWTHGGRYLLYDIFGNKFEVTNKYQPPIMPIGRGAYGIVCSVMNFETREMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gapa
                                                                    phytohormone expression, including ethylene, auxins, and gibberellin, to provide control of plant response to
                                                      encoded proteins useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 72.9%; Score 1423; DB 4;
Best Local Similarity 72.3%; Pred. No. 3.4e-137;
Matches 263; Conservative 50; Mismatches 49;
                                                        nucleic acids and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW15513 standard, protein, 423 AA.
                                                                                                                                                     Claim 13; Page 94; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                        transduction
phytohormone
                                                                                                                 environmental stresses.
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                    N-PSDB; AAC84262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 398 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAP kinase #2.
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                                                                            regulating
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The invention describes a recombinant DNA construct comprising a polymucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at available in electronic form from the US patent office at the polymucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lighin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, initrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one struction of content. This is the amino acid sequence of a plant full length insert polypeptide that can be used in the recombinant DNA construct of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172 ANCDLKICDFGLARPSSESDMMTEYVVTRWYRAPELLLNSTDY-SAADVWSVGCIFMELI 230
         plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; heat tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; yalatonannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 DVYIATELMDTDLHHIIRSNQELSEEHCQYFLYQILRGLKYIHSANVIHRDLKPSNLLLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52 SVMNPETREMVAIKKIANAFNNDMDAKRTLREIKLLRHLDHENIIGIRDVIPPPIPQAFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68.6%; Score 1340.5; DB 8; 77.1%; Pred. No. 7.7e-129; ive 46; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 49119; 15pp; English.
                                                                                                                                                                                                                                                                              28-APR-2003; 2003US-00425114
                                                                                                                                                                                                                                                                                                                06-MAY-1999; 99US-00304517
05-NOV-2001; 2001US-00985678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhou Y, Kovalic DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity ''...
Matches 242; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   ZHOU Y.
KOVALIC D K.
SCREEN S B.
TABASKA J E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-180133/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pests, for conferment improving yield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 318 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAO Y.
                                                                                                                                                                          Unidentified.
                                                                                                                                                                                                                                             19-FEB-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                   (LIUJ/)
(ZHOU/)
                                                                                                                                                                                                                                                                                                                                                                                                                                          (TABA/)
(CAOY/)
                                                                                                                                                                                                                                                                                                                                                                                                                        SCRE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu J,
                                                                                                                                                                                                                                                                                                                                                                                                       (KOVA/)
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                                                                                                                                                                                                                                                                                                                                                                                                    AAWISSI2 and AAWISSI3 represent the mitogen activated protein (WAP) kinases of the invention. This sequence contains the T-E-Y sequence, in which the threonine and tyrosine residues are phosphorylated to activate the protein at residues 249-251. The WAP kinase and its gene can be used to regulate the synthesis of jasmone acid and the synthesis of a group of infectious specific proteins. By introducing the MAP kinase gene into a plant, thereby inducing expression of the mRNA for MAP kinase gene into a plant, thereby inducing expression of the mRNA for MAP kinase (or its antisense RNA), the synthesis of jasmone acid and a group of infectious specific proteins can be regulated in the plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 EEHCOYFLYOILRGLKYIHSANVIHRDLKPSNLLLANANCDLKICDFGLARPSSESDMMTE 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YVVTRWYRAPELLLNSTDYSAA-DVWSVGCIFMELINROPLFPGRDHMHOMRLITEVIGT 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIDDELGFIRNEDARKYMRHLPQYPRRTFASMFPRVQPAALDLIERMLTFNPLQRITVEE 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGRYLLYDIFGNKFBVTNKYQPPIMPIGRGAYGIVCSVMNFBTREMVAIKKIANAFNNDM 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DAKRTLREIKLLRHLDHENIIGIRDVIPPPIPQAFNDVYIATELMDTDLHHIIRSNQELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251 YVVTRWYRAPELLINSSDYTAAIDVWSVGCIFWELMNRKPLFAGKDHVHQIRLLTELLGT
                                                                                                                                                                                                                                                                                                                  Wound-stress inducible MAP kinase - used to regulate the synthesis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
Mitogen activated protein kinase; MAP; infectious specific protein;
plant; jasmone acid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70.7%; Score 1380.5; DB 2; Length 423; 72.3%; Pred. No. 8.8e-133; tive 51; Mismatches 41; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant full length insert polypeptide segid 49119.
                                                                                                                                                                                                                               (NORQ ) NORINSUISANSHO NOGYO SEIBUTSU SHIGEN
                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 16-17; 21pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADX79753 standard; protein; 318
                                                                                                                                                        95JP-00220935
                                                                                                                                                                                            95JP-00220935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 72.34
Matches 253; Conservative
                                                                                                                                                                                                                                                               WPI; 1997-220416/20.
N-PSDB; AAT60350.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 423 AA;
                                                                                                                                                                                            29-AUG-1995;
                                                                                                                                                                                                                                                                                                                                    jasmone acid
                                                                                                                         11-MAR-1997
                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a rice mitogen-activated protein kinase 5
(MARKS) polypeptides and the polymucleotides encoding them. The invention
also relates to an antibody that specifically binds to a peptide
consisting of a C-terminal portion of a MARKS polypeptide, a transgenic
c plant transformed by a polymucleotide encoding a MARKS orthologue where
cover expression of the MARKS orthologue in the plant results in increased
tolerance to abiotic stress compared to a wild-type plant and a method
for evaluating a plant for tolerance to abiotic stress comprising
for evaluating a plant with abiotic stress, isolating a MARKS protein from the
plant, detecting MARKS activity and evaluating the increase or decrease
in MARKS activity in the plant where the increase in MARKS activity
indicates the plant is tolerant to abiotic stress. The methods and
compositions of the present invention are useful for increasing tolerance
to abiotic and biotic stress in plants using MARKS, where the abiotic
stress is drought, temperature or salinity and the biotic stress is from
                                                                                                  NROPLFPGRDHMHOMRLITEVIGTPTDDELGFIRNEDARKYMRHLPQYPRRTFASMFPRV 290
                                                                         241
SNCDLKIIDFGLARPTLESDFWTEYVVTRWYRAPELLINSSDYTSAIDVWSVGCIFWELM 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid molecule encoding a mitogen-activated protein kinase-5 (MAPK5) polypeptide, useful for increasing tolerance to abiotic and biotic stress in plants.
                                                                                                                                                                                                                                                                                                                                                                          Rice; mitogen-activated protein kinase 5b; MAPK5; MAPK5b; abiotic stress tolerance; biotic stress tolerance; temperature;
                                                           Rice mitogen-activated protein kinase 5b (MAPK5b) polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .3
/note= "Encoded by ATGGAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 12; SEQ ID NO 4; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                            ADT02332 standard; protein; 266 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-JAN-2003; 2003US-0444249P
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IKEMIYREALALNP 315
                                                                                                                                                            MKQLIFNEAIEMNP 364
                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                        salinity; plant; enzyme.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yang Y, Xiong L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (YANG/) YANG Y. (XION/) XIONG L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ADT02331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa
                                                                                                                                                                                                                                                                                                                    13-JAN-2005
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                                                                                                                                                                                    302
                                            231
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61 MVAIKKIANAFNNDMDAKRTLREIKLLRHLDHENIIGIRDVIPPPIPQAFNDVYIATELM 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DHMHOMRLITEVIGTPTDDELGFIRNEDARKYMRHLPQYPRRTFASMFPRVQPAALDLIE 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DHMHQMRLITEVIGTPTDDELGFIRNEDARKYMRHLPQYPRRTFASMPPRVQPAALDLIE 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RMLTFNPLORITVEEALDHPYLERLHDIADEPICLEPFSFDFEOKALNEDOMKOLIFNEA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------ ANCDLKICD 77
                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                    MDGAPVAEFRPTWTHGGRYLLYDI FGNKFEVTNKYQPPIMPIGRGAYGI VCSVMNFETRE
                                                                                                                                                                                                                      1 MDGAPVAEFRPTWTHGGRYLLYDIFGNKFEVTNKYQPPIMPIGRGAYGIVCSVMNFETRE
                                                                                                                                                                                                                                                                                                                                                                                                                 121 DTDLHHIIRSNQELSEEHCQYFLYQILRGLKYIHSANVIHRDLKPSNLLLNANCDLKICD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FGLARPSSESDMMTEYVVTRWYRAPELLLNSTDYSAA-DVWSVGCIFMELINRQPLFPGR
                                                                                                                                                                         Gaps
pathogenic bacteria, viruses, nematodes and insects. This sequence represents the rice MAPK5b polypeptide of the invention.
                                                                                                                                                                         0; Indels 105;
                                                                                                                         Length 266;
                                                                                                                         DB 8;
                                                                                                                      68.3%; Score 1334.5; DB 8 71.5%; Pred. No. 2.5e-128; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: December 27, 2005, 20:36:29 Job time : 191 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 264; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         258 IEMNPNIRY 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            360 IEMNPNIRY 368
                                                                                                                                               Local Similarity
                                                                         Sequence 266 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            198
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                                                                                                                         Query Match
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score:

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Scoring table:

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Database

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ARI10410 Cyrza sat ARI15910 Cyrza sat ARI53061 Pisum sat ARI49424 Ipomocae b X82270 M.sativa MM D21842 Arabidopsis AX048762 Sequence AX505949 Sequence BT0008655 Arabidops AR0505913 Arabidops AR30508141 Chlamydom D21839 Arabidopsis AY173962 Triticum AR247135 Capsicum DQ078119 Rheum aus AB098729 Nicotiana AR261514 Lycopersi Y12748 Sequence U94192 Nicotiana Cylly Capsicum AR01848 Sequence U94192 Nicotiana Cylly Capsicum AR0186805 Sequence U94192 Nicotiana Cylly Capsicum AR0186805 Sequence U94192 Nicotiana Cylly Capsicum AR0186805 Sequence
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Bhrhartoideae, Oryzae, Oryza.

I (bases 1 to 1396)
Xiong, L. and Yang, Y.
Xiong, L. and Yang, Y.
Disease Resistance and Abiotic Stress Tolerance in Rice Are
Inversely Modulated by an Abscisic Acid-Inducible Mitogen-Activated
Protein Kinase
                                                                                                                                                                                                                                                                                                                             Oryza sativa MAP kinase MAPKSa (WAPKS) mRNA, complete cds, alternatively spliced.
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/note="blast fungus and ABA-inducible; alternatively
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Xiong,L., Qi,M. and Yang,Y.
Molecular cloning and characterization of a novel MAP kinase,
Unpublished
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AY261514
PCMAPKINA
                                AF149424
MSMMK4
ATHATMPK6
                                                                                                              AB035141
ATHATMPK3
                                                                      AX048762
AX048758
AX505949
BT008855
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AF247135
DQ078119
AB098729
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NTU94192
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BT000007
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/db_xref="taxon:4530"
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/note="OBMAPK5"
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     AL250311 Oryza sat
AK104834 Oryza sat
AK104834 Oryza sat
AF332873 Oryza sat
AJ486975 Oryza sat
AY738652 Saccharum
AF079318 Triticum
X79993 A. sativa AS
AX048754 Sequence
AK47984 Oryza sat
AB016801 Zea mays
AK642433 Brassica
AK111942 Oryza sat
AK111942 Oryza sat
AK111942 Oryza sat
AK111942 Oryza sat
AK11942 Oryza sat
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AF216315 Oryza sat
                                                                       December 29, 2005, 04:38:30 ; Search time 4832 Seconds (without alignments) 16422.487 Million cell updates/sec
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                                                                                                                                   1 agagagtcagataaggtcgt..........
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              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                  5883141 seqs, 28421725653 residues
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AK067339
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AF216315
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AXO48754
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AB016801
AY642433
AY805424
AX111942
AB183398
OSA535841
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Maximum Match 100%
Listing first 45 summaries
                                                     using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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1 (bases 1 to 1396)
Wen, J.Q., Oono, K. and Imai, R.
Two Novel Mitogen-Activated Protein Signaling Components, OsMEX1 and OsMAPI, Are Involved in a Moderate Low-Temperature Signaling Pathway in Rice
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DWSKYGCIFMELINRQPLFPERBHHHQMRLITEWIGTPTDBLGFIRNBDARKYMRHL
PQYPRRTFASMFPRVQPAALDLIERMLTFNPLQRITVEEALDHPYLERLHDIADBFIC
LEPFSFDFEQKALNEDQMKQLIFNBAIEMNNIRY"
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100.0%; Pred. No. 5.6e-185;
ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 1396; Conservative
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Cryza sativa mRNA for MAPK2 protein (mapk2 gene).
AJ250311.
AJ250311.1 GI:10862875
Mapk2 gene; MAPK2 protein.
Cryza sativa
Oryza sativa
Oryza sativa
Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryzea.
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Unpublished
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2 (bases 1 to 1457)
Huang, H.J.
Direct Submission
Submitted (15-OCT-1999) Huang H.J., Department of Biology,
Cheng-Kung University, 1, University Rd., Tainan 701, TAIWAN
Location/Qualifiers
1457
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Molecular Cloning of a Low Temperature-Inducible
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note="protein kinase; MAP1"
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The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kikuchi, S., Satoh, X., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo, Y., Murakami, K., Ilda, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J.,
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza, y Vitdiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Enhrhartoideae; Oryzeae;
                         CGGCCGCCATCGACGTCTGGTCCGTCGGCTGCATCTTCATGGAGCTCATCAACCGCCAGC
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                                                                                                 Length 1411;
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                                                                                                    DB 15;
                                                                                                                               Pred. No. 3e-182;
                                                                         Best Local Similarity 99.9 Matches 1377; Conservative
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12860'10., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fylimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, M., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hayashida, K., Hayashidaki, Y., Ishaka, R., Imamura, K., Ishibki, J., Ishi, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Murata, M., Nagata, T., Makamura, M., Namuka, M., Namuka, R., Mikura, J., Nishi, K., Nomura, M., Namuka, R., Nishi, K., Nomura, M., Namuka, R., Ohneda, E., Satoh, H., Sakai, C., Sakai, C., Sahaia, T., Tagama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami, Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Yanada, H., Yanada, H., Yanamanoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yanada, H., Yanamanoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yanada, E., Manada, H., Yanamanoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yanada, E., Manada, H., Yanamanoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yanada, E., Manada, H., Yanamanoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yanada, H., Yanada, M., Yanada, Yanada, M., Yanada, Y
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rice.
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Collection, mapping, and annotation of over 28,000 cDNA clones from
Science 301 (5631), 376-379 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission

Direct Submission

Submitted (27-ARO2202) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki Cals. 181-129-898-7007, Res. 81-29-838-7007, This clone is one of the 28K full-length cDNA clones from japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Oryza sativa (japonica cultivar-group)"
| Mol type="mRNA"
|cultivar="Nipponbare"
| db_xref="taxon:39947"
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REFERENCE
AUTHORS
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JOURNAL
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COMMENT

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VILLE. http://cdnaol.dna.affrc.go.jp/cDNA/
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Towanishi,A. and Hayashizaki,Y.
Towanishi,A. and Hayashizaki,Y.
Towanishi,A. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@mis.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007) This clone is one of the 28K full-length cDNA clones from japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 AGGAGGAGTTAGGGATGGACGGGCGCCGGTGGCGGAGTTCAGGCCGACGATGACGC 120
Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M.,
Namiki, T., Narikawa, R., Niikura, J., Nishi, K., Nomura, K.,
Numasaki, R., Ohneda, B., Ohno, M., Ohteuki, K., Oka, M., Ooka, H.,
Osato, N., Ota, Y., Otomo, Y., Ryu, R., Saltoh, H., Sakai, K.,
Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K.,
Shinagawa, A., Suriki, T., Shishiki, T., Sogabe, Y., Sugano, S.,
Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y.,
Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A.,
Toya, T., Taunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W.,
Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113 AGAGAGTCAGATAAGGTCGTTAATTAGGTTGTCAATTCGGCTGCTTGCGGCGGAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           173 AGGAGGATTAGGGATGGACGGGCGCCGTGGCGGGGGGGCGAGTTCAGGCCGACGATGACGC
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99.9%; Pred. No. 3e-1:
ive 0; Mismatches
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/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="J013102017"
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                                                                                                                                                                                                                                                                                                                                                                                                                    Yoshimura, A.
Direct Submission
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa (japonica cultivar-group) cDNA clone:J013102017, full insert sequence.
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                                                                                           AGGCGCTCGATCATCCTTACCTAGAGATTGCACGACATCGCCGATGAGCCCATCTGCC 1080
                                                                                                                                         1054 AGGGGTTCGATCATCCTACCTAGAGAGATTGCACGACATCGCCGATGAGCCCATCTGCC 1113
                                                                                                                                                                                                                                                          1081 TGGAGCCCTTCTCCTTCGACTTCGAGCAGAGGCTCTAAACGAGGACCAAATGAAGCAGC 1140
                                                                                                                                                                                                                                                                                                       1114 TGGAGCCCTTCTCCTTCGACTTCGAGCAGAAGGCTCTAAAACGAGGACCAAATGAAGCAGC 1173
                                                                                                                                                                                                                                                                                                                                                                                                                1141 TGATCTTCAACGAAGCGATCGAGATGAACCCAAACATCCGGTACTAGATTGAATCACCAT 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1174 TGATCTTCAACGAAGCGATCGAGATGAACCCAAACATCCGGTACTAGATGAATCACCAT 1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGAAATGAGATCCCGTCTATACCTGCTTTGTACATATGATCAAGATTGAGAGCCGGGTAG 1260
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                994 CGCTCGACCTCATCGAGAGGATGCTCACCTTCAACCCGCTGCAGAGAATCACAGTTGAGG 1053
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa; Oryza sativa; Suponica cultivar-group)
Bukaryota; Viridiplantae; Strepcophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1321 GCTGCTTTGTATGATATATGGTACTATGTTCGAATAAAAGGGTTTGGAACTTTGGATT 1378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1354 GCTGCTTTGTATGTATATGGTACTATGTTCGAATAAAAGGGTTTGGAACTTTGGATT 1411
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VERSION
KEYWORDS
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| Oy 1321 GCTGCTTTGTATGATATATGGTACTATGTTCGAATAAAGGGTTTGGAACTTTGGATT 1378<br> | 6<br>73<br>TION<br>ION<br>N<br>DS                                   | SOURCE Oryza sativa (indica cultivar-group) ORGANISM Oryza sativa (indica cultivar-group) ENKAryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta; Spermatophyta, Magnollophyta; Liliopsida, Poales, Poaceae; | REFERENCE 1 (Dases 1 to 1424) AUTHORS Song, F. and Goodman, R.M. TITLE OSBIMEN, a novel MAP kinase from rice that is involved in systemic | JOURNAL Unpublished RelBeance REFERENCE 2 (bases 1 to 1424) AUTHORS Song, F. and Goodman, R.M. | S AL                                                            | <pre>Bource</pre>                                                    | / where = caxon: 59345<br>/ dev stage="seedling"<br>991208<br>/ codon starts = 15000 BTWF1 | /product="white binkl" /protein_id="AAKO110.1" /db_xref="GI:12698976" /db_xref="MOGAPVAERPTWTHGGRYLLYDIFGNKFBVTNKYOPPIMPIGR | GATGLESOWING TERMINATION TO THE AUGUST THE AUGUST TO SECUL  PPP I POPTED THE THE THE TOTAL THE AUGUST THE AUGUST THE AUGUST TO SECUL  RDLKPSNLLLNANCDLKI CDFGLARPSSESDWITEYVUTWYRAYRAPELLLNSTDYSAAI  DVWSVOCT PIWELI NRQPLFPRORICELITEVI GTFP TOBLEGET RNEDRAKYWHHL  POVAPDPRES AWDRONGON TON TON TON THE THE THEORY THE PROBLEM TO HEVE THE TO THE POPUL THE PROBLEM TO THE PROBLEM TO THE PROBLEM THE PROBLEM TO THE PROB | LEPFSFDFEQKALNEDQMKQLIFNEAIEMPNFRY"  ORIGIN                             | Query Match 98.5%; Score 1375.2; DB 15; Length 1424;<br>Best Local Similarity 99.6%; Pred. No. 4.46-182;<br>Matches 1390; Conservative 0; Mismatches 3; Indels 3; Gaps 1; | Oy 1 AGAGAGTCAGATAAGGTCGTTAATTAGGTTGAATTCGGCTGCTGCGGCGAGAGG 60                                                                                                                                                       | QY         61 AGGAGGAGTAGGGATGGACCCCGCCGCTCGTCGGAGTTCAGGCCGACGATGACGC 120                                                                                                                           | OY 121 ACGGCGGCCGGTACCTGCTCTACGGCAACAAGTTCGAGGTGACGAACAAGT 180                                                                                                  | Oy 181 ACCAGCCGCCATCATGCCCATTGGCCGCGCGCCTACGGGATCGTCTGCTCCGTGATGA 240                 | OY 241 ACTTTGAGAGGAGATGGTGGCGATAAAGAAGATCGCCAACGCGTTCAACAACGACA 300 | Qy 301 TGGACGCCAAGGCTCCGGGAGATCAAGCTCCTCAGGCACCTCGACCACGAGAACA 360 |
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/ codon start=1
/ product==MAP Kinase=
/ db xref==GI:20975736=
/ db xref==GOA:Q7FNE2=
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/ db xref==InterPro:1PR003527=
/ db xref==InterPr
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Oryza sativa (japonica cultivar-group) mRNA for MAP Kinase (msrmk2
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AJ486975.1 GI:20975735
MAP Kinase; msrmkz gene.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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Isolation of novel rice (Oryza sativa L.) multiple stress responsive MAP kinase gene, OsMSPAKZ, whose mRNA accumulates rapidly in response to environmental cues Blochem. Blophys. Res. Commun. 294 (5), 1009-1016 (2002) 12074577
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/mol type="mRNA"
/cultivar="Nipponbare"
/tissue f="taxon:39947"
/tissue type="leaf"
/dev stage="two-week-old seedling"
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Direct Submission
Submitted (11-MAY-2002) Agrawal G.K., Biotechnology and
Biochemistry, Research Lab. for Agri. Biotech. and Biochem.
(RLABB), GPO 8207, Kathmandu, NEPAL
mRNA.
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Best Local Similarity 100.0%; Pred. No. 2.9e-179;
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ENGARVARANPDNHMDAKRTLREIKLLRHLDHENIIGIRDVI
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2NVAALDLIARPSSESDMYTEVYPRWYRAPBELLINSTOYSAAI
2NVAALDLIERMLTPNPLQRITVEEALEHPYLERLHDIADEPI
EDQWKQLIFNBAIEWNPNFRY" TIGLEGCTGCTTTGTATGATATATGGTACTATGTTC 1351 treptophyta; Embryophyta; Tracheophyta; a; Liliopsida; Poales; Poaceae; PACCAD goneae; Saccharum; Saccharum officinarum 3 bp mRNA linear PLN 14-JUN-2005 en-activated protein kinase mRNA, CCATGGAAATGAGATCCCGTCTATACCTGCTTTGT 1201 TCAGGCCGACGATGACGCACGGCGGCCGGTACCTG 137 S., Camargo, S.R., Fernandez, J.H., De P. and Arruda, P. Comain protein family, is associated ca stress in sugarcane (2005) EG, UNICAMP, Zeferino Vaz/sn, Campinas, S., Camargo, S.R., Fernandez, J.H., De P. and Arruda, P. 3; Gaps 935.4; DB 15; Length 1113; No. 8e-121; smatches 101; Indels 3; ||||||||||| TTAAAAAAA 1356 TTAAAAAAA 1386 um officinarum" 80" 00

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DOWSVGCI PRELINRAPLFPERDHMMIQMELTEVIGFPDDDDJGFIRNEDARRYMRHL
POPPRASPEGGFPRVQDAALDLIERMLTFWELGRITVEEALEHPYLERLHDVADEPIC
TDPPSFDFEGHPLTEDQMKQLIFNEALELNPNFRY"
                                                        Triticum aestivum (bread wheat)
Triticum aestivum
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Pooideae, Triticeae, Triticum.
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Submitted (21-JUL-1998) Basic Cryoscience, Institute of
Temperature Science, Hokkaido University, Kita 19 Nishi
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   mRNA,
 (WCK-1)
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112. .1221
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2 (bases 1 to 1520)
Huttly,A.K.
Direct Submission
Submitted (30-JUN-1994) A.K. Huttly, Institute of Arable Crops
Research, Univ. of Bristol, Dept of Agricultural Sciences, Long
Ashton Research Station, Bristol, BS18 9AF, UK
Location/Qualifiers
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Pred. No. 2e-119;
0; Mismatches 118; Indels
                                                                                                                 /organism="Avena sativa"
|mol type="mRNA"
|cultiva=="Athannon"
|db xref="taxnon:4498"
|clone="ASMAP1"
|tissue type="Aleurone"
|clone lib="aleurone cDNA"
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rta; Liliopsida; Poales; Poaceae;
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                  CGTCTACATCGCCACGGAGCTCATGGACACCGACCTCCATCACATCACCGCCCCAACCA
                                   CGTCTACATCGCCACTGAGGTCATGGACACGGACCTCCACCACATCATCCGCTCCCAACCA
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MAP Kinase; serine/threonine protein kinase.
Avena sativa (oat)
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Plant Mol. Biol. 27 (5), 1043-1052 (1995)
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Spermatophyta; Magnoliophyta;
Pooideae; Aveneae; Avena.
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0; Mismatches 127;
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Matches 992; Conservative
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Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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/organism="Zea mays"
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                                                                     GAACGCCAACTGCGACCTCAAGATCTGCGACTTCGGGCTGGCGCGCCGTCGTCGGAGAG
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/product="WAP Kinase MAPK5b"
/protein_id="AAL87690.1"
/protein_id="AAL87690.1"
/db_xref="G1:19401854"
/translation="MDGAPVAEFRPTWTHGGRYLLYDIFGNKFBVTNKYQPPIMPIGR
GAYGIVCSWNWPETRENVAIKKIANCPLKICPFGLARPSSESDMYTEXVYTRWYRAPE
LLLNSTDYSAAIDWWSVGTFWELINRQPLFRGFRDHHQMRLITEVIGTPTDDELGFI
RNEDARKYMRHLPPYPERTFAEMPFRYQPAALDLIERWLTFRPLQRITVEEALDHPYL
ERLHDIADEPICLEPPSFDFEQKALNEDQMKQLIFNEAIEMNPNIRY"
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1. (bases 1 to 1044)

Xiong, L. and Yang, Y.
Disease Resistance and Abiotic Stress Tolerance in Rice Are
Inversely Modulated by an Abscisic Acid-Inducible Mitogen-Activated
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AF479884.1 GI:19401853
                                                                                                                                                                     GAGCACCCGTACCTGGAACGGCTACACGACGACGCCGACGACGACCCATCTGCACGGACCGC 1026
                                                                                                                                                                                                                                                                996
  CAGTICCCGCGCCGGCCGTTCGTCAGCCTGTTCCCGCGGATGCAGCCCGTCGCGCTGGAC 906
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Xiong,L., Qi,M. and Yang,Y.
Xiong,L., Qi,M. and Characterization of a novel MAP kinase,
Molecular cloning and characterization of a novel MAP kinase,
OswaPKS, in rice
Unpublished
J (based to 104)
Xiong,L., Qi,M. and Yang,Y.
Direct Submission
Submitted (01-FEB-2002) Plant Pathology, University of Arkansas,
217 Plant Science Bulliding, Fayetteville, AR 72701, USA
                                              CTCATCGAGAGGATGCTCACCTTCAACCCGCTGCAGAGAATCACAGTTGAGGAGGCGCTC
                                                                            CTCATCGAGCGGATGCTCCACCTTCAACCCGCTGCAGAGGATCACAGTGGAAGAGGCGCTG
                                                                                                                                          GATCATCCTTACCTAGAGAGATTGCACGACATCGCCGATGAGCCCATCTGCCTGGAGCCC
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| Corganiam="Oryza sativa"

| Mol_type="mRNA"

| db_xref="taxon:4530"

| 1. | 1084

| 1. | 29ne="MAPKS"

| note="08MAPKS"

| 78. :875
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mRNA linear PLN 06-JUL-2005 mitogen-activated protein kinase 3
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Brassica napus
Brassica napus
Brassica napus
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicace; Brassica.
1 (bases 1 to 1464)
Yu,S., Zhang,L., Zuo,K., Tang,D. and Tang,K.
Isolation and characterization of an oilseed rape MAP kinase BnMPK3 plant Sci. 169 (2), 413-421 (2005)
2 (bases 1 to 1464)
                                                                                                                                                                                                                                                                                                                                              GCTGCATCTTCATGGAGCTCATCAACCGCCACCGCTCTTCCCCGGACGCGACCACATGC
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   ACCAGATCCTCCGCGGGCTCAAGTACATCCACTCCGCCAACGTGATCCACGTTGACCTCA
                                     <u> AGCCGAGCAACCTGCTGCTGAACGCCCAACTGCGACCTCCAAGATCTGCGACTTCGGGGCTGG</u>
                                                                                                                                                                        CGCCGGAGCTGCTGAACTCCACCGACTACTCCGCCGCCATCGACGTCTGGTCCGTCG
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Direct Submission
Submitted (01-JUN-2004) Agriculture and Biology,
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Braselca napus cultivar Huyou15
mRNA, complete cds.
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PVMPTGRGAYGIVCSVMNPETREMVAIKKIANAFDNHMDAGRTLREIKLIEHLAHLDHBNI
IGIRDVIPPPPVPQARNDYIGTELMDYDLHHIIRNOBLESEBISQYFLYQILRGLKYI
HSANVIHYDLKPSNILJUNANCDLKICPFGLARPSSBSDMYTEYVYTRWYRAPELLIUN
IDYSAAIDVWSVGCIFMELINRQPLFPGRDHMHQMRLITEARVTHATHPTSPSYNSIP
SSSAANNITAARQVIGTPTDDELGFINRDARKYMRHLDQFPRRPFYSLFPRNQPVALD
LIERWLTFNPLQRITVUSRALEHPYLERLHDVADEPICTDPFSFDFEQQALTEDQMKGL
IFNRAIELNPNFRY
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                       senescence and recovery
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                                                                                                                     Direct Submission
Submitted (07-AUG-1998) Tomonobu Kusano, Nara Institute of Sci
and Technology, Research and Education Center for Genetic
Information; 8916-5 Takayama-cho, Ikoma, Nara 630-0101, Japan
Ramil;kusano@bs.aist-nara.ac.jp, Tel:81-743-72-5651,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 800.8; DB 15;
Pred. No. 4.2e-102;
0; Mismatches 127;
Berberich, T., Sano, H. and Kusano, T. Involvement of a MAP kinase, ZmMPK5, in Elem low-temperature stress in maize Mol. Gen. Genet. 262 (3), 534-542 (1999) 10589842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="BAA74733.1"
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/db xref="taxon:4577"
/clone="ZmMPK4"
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1. .1647
                                                                                                                                                                                                                                                                                                                                                                                                                                                   'product="MAP kinase
                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                              /gene="ZmMPK4"
139. .1359
/gene="ZmMPK4"
/codon_start=1
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Best Local Similarity 81.8%;
Matches 977; Conservative
                                                                                       (bases 1 to 1647)
                                                                                                       Кивапо, Т
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/translation="MNAGGQFTDFPAVQTHGGQFISYDIFGSLFEITSKYRPPIIPIG
RGAYGIVCSVLDSETNELVAMKKIANAFDNHMDAKRTLREIKLLRHLDHENIIAIRDV
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IDVWSVGCIFMELMNKFLFPGKDHVHQMRLITELLGTPTESDLGFTHNEDAKRYIRQ
LPSFPRQPLAALFSHVPLAADLVDRMLITPDNRRITVEEALNHQYLAKLHDPNDEPI
CQKPFSFEFEQQPMDVEQIKEMIYKEAIALNPTYG"
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Chorispora bungeana mitogen-activated protein kinase 3 (mpk3) mRNA,
complete cds.
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P.R.China
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                                                                                          834 ATCGGGACGCCGACGGACGACGACGTGGGGTTCATACGGAACGAGGACGCGAGGAAGTAC
                                                                                                                                                                                ATGAGGCACCTGCCGCAGTACCCGCGCCGGACGTTCGCGAGCATGTTCCCGCGGGTGCAG
CGCCAGCCGCTCTTCCCCGGCAGGGACCACATGCACCAGATGCGCCTCATCACCGAGGTG
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/product="mitogen-activated protein kinase
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAV68711.1"
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AY805424.1 GI:55978181
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92. .1201
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IHRDIKPSNLLLNANCDLKT CDFGLARPTSENBFMTEXVVTRWYRABELLNSSDYTA
ATTENWAVGCT FMELMNRKPLEPEKORPHYGMRLLTELLGTPTESDLGFTHNEDAKRYIR
QLPRFPRQFLAKLFERHVNSLAIDLVDRMLTFDPNER ITVEBALNHPYLAKLHDPNDEP
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grgaygivcsvldsetnelvamkkianafdnihddakrtlreikllerhldhenilaird
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Biotechnology Research Center, 1954# Huashan Road, Shanghai 200030,
China
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTGATGAACTTTGAGACGAGGGAGATGGTGGCGATAAAGAAGATCGCCAACGCGTTCAAC 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AACGACATGGACGCCAAGCGCACGCTCCGGGAGATCAAGCTCCTCAGGCACCTCGACCAC 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGAACATCATAGGCATCAGGGATGTGATCCCGCCGCCGATCCCTCAGGCGTTCAACGAC 413
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Pred. No. 5.2e-71;
0; Mismatches 339; Indels 0;
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                                                                                                                                                                                                                                                             /product="mitogen-activated protein kinase
/protein_id="AAV34677.1"
/db_xref="GI:54402040"
                                                                 1. .1464
/organism="Brassica napus"
                                                                                                                                                                            154. .1266
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environmental stresses"
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/db_xref="taxon:3708"
154_.1266
                                           Location/Qualifiers
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Best Local Similarity 69.7%;
Matches 781; Conservative (
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| 23 Similarity 773 Conservat. 59 AdaGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG | 58.4%; Pred. No. 2.2e-68; Indels 0; Gaps 0; | 59 AGAGGAGGAGGATTAGGACGGGGGCGCCGGTGGCGGAGTTCAGCCCGACGATGAC 118 | 76 ATAGAGAGAGAAAGATGAAGCGCCGGCGGCCAGTTCACAGATTTCCCGGCGGTGCAAC 135 | 17                            | TCATGGAGGACAGTTCATAAGTTACGATATCTTCGGTAGTCTATTCGAGATCACATCCAA 195 | ω.                            | SATCATACCAATCGGCCGCGGCGCATATGGAATCGTATGCTCCGTGTT 255 |  | SAACGAGCTGGTGGCGATGAAGAAGATAGCGAACGCCTTCGATAATCA 315 | CATGGACGCAGGCACGCTCCGGGAGATCAAGCTCCTCAGGCACCTCGACAA 358  CATGGACGCAGGCAACGCTCCGGGAGATCAAGCTCCTCAGGCACCTCGAGAA 358  CATGGACGCCAAGCGTACAAGACAAGAAAAAA 375 |  | SCTCATGGACACCGCCCCATCATCCGCTCCAACCAAGAACT 478 | TATTGCGACTGAACTAATGGACACTGATCTTCATCAAATCATCAGATCCAACCAGAGTTT 495 | GTCAGAAGAGCACTGCCGGTATTTCCTGTACCAGATCCTGCGGGGGGCTCAAGTACATCCA 538 | TITITITITITITITITITITITITITITITITITITI | CTCGGCGAACGTGATCCACCGCGACCTGAAGCCGAGCAGCTGCTGCTGAACGCCAACTG 598 | TATTCACAGGGATTTAAAGCCAAGCAATCTTCTCCTGAACGCAAATTG 615 | CGACCTCAAGATCTGCGACTTCGGGCTGGCGGGCCGTCGTCGGAGAGCGACATGATGAC 658 | ETGCGATTICGGICTIGCTAGACCAACTICAGAGAACGAGITTATGAC 6/5 |  | GACGICIGGIC CGICGGCIGCATCTICATGGAGCTCATCAACGCCCA 778 |  | ω : | GALGECCEARCGAACGAAGGAGGTICATACGGAAACGAGGAGGAAGGAAGTACATGAG BYB | 95 | 9 | CATCGAGAGGATGCTCACCTTCAACCCGCTGCAGAGAATCACAGTTGA 1018 |  | 7 | CCACCAGTACCTAGCCAAATTGCACGACCCAAATGATGAGCCAATCTG 1095 | CCTGGAGCCCTTCTCCTTCGACTTCGAGCAGAAGGCTCTAAACGAGGACCAAATGAAGCA 1138 |
|-------------------------------------------------------------------------|---------------------------------------------|----------------------------------------------------------------|-------------------------------------------------------------------|-------------------------------|------------------------------------------------------------------|-------------------------------|------------------------------------------------------|--|------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------|--|-----------------------------------------------|------------------------------------------------------------------|-------------------------------------------------------------------|----------------------------------------|-----------------------------------------------------------------|------------------------------------------------------|-----------------------------------------------------------------|------------------------------------------------------|--|------------------------------------------------------|--|-----|----------------------------------------------------------------|----|---|-------------------------------------------------------|--|---|-------------------------------------------------------|-------------------------------------------------------------------|
|                                                                         | milarity 68.4%;<br>Conservative 0           | 59 AGAGGAGGAGGATTAGGGATGGAC                                    | 76 ATAGAGAGAGAAAAGATGAACGCC                                       | 119 GCACGGCGGCCGGTACCTGCTCTAC | 136 TCATGGAGGACAGTTCATAAGTTAC                                    | 179 GTACCAGCCGCCCATCATGCCCATT | 196 GTATCGCCTCCGATCATACCAATC                         |  | 256 GGATTCGGAGACGAACGAGCTGGTG                        |                                                                                                                                                         |  | 419 CATCGCCACGGAGCTCATGGACACC                 | 436 TATTGCGACTGAACTAATGGACACT                                    | 479 GTCAGAAGAGCACTGCCAGTATTTC                                     | 496 GTCAGAGGAGCACTGTCAGTACTTC          |                                                                 | 556 CTCGGCTAACGTTATTCACAGGGAT                        |                                                                 |                                                      |  | 719 crecececerceacerereer                            |  |     |                                                                |    |   | 959 cececreacercareaagare                             |  |   |                                                       | 079 CCTGGAGCCCTTCTCCTTCGACTTC                                     |

Db 1096 TCAAAAGCCATTCTCTTTTGAGTTCGAACAACAGCCTATGGACGTGGAACAGATAAAAGA 1155
Qy 1139 GCTGATCTTCAACGAAGCGATCGAGATGAACCCAAACATCCGGTACTAGA 1188
Db 1156 GATGATCTACAAAGAAGCCATTGCACTCAATCCAACATATGGTTAGAAGA 1205

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